

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96021

To: Mary Schmidt
Location: CM1-11E12
Art Unit: 1635
Monday, June 16, 2003

Case Serial Number: 09/532001

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

)

STIC-Biotech/ChemLib

96021

From: Hutzell, Paula
Sent: Friday, June 06, 2003 12:01 PM
To: Schmidt, Mary; STIC-Biotech/ChemLib; Chan, Christina
Subject: RE: RUSH sequence search request 09/532,001

approved

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:59 AM
To: Hutzell, Paula
Subject: FW: RUSH sequence search request 09/532,001

CRF

Hi, according to Christine's out of office message, we should send rush requests to you...

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:57 AM
T : Chan, Christina
Subject: FW: RUSH sequence search request 09/532,001

Hi, do you submit sequence search requests? Jeff and Jim are out of the office. If not, could you let me know who else does?

thanks,
Melissa

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:56 AM
T : Martinell, James
Subject: FW: RUSH sequence search request 09/532,001

Hi, Jeff is out today, if you are in, could you submit?
thanks,
Melissa

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:55 AM
To: Fredman, Jeffrey
Subject: RUSH sequence search request 09/532,001

I missed a sequence in the claims and this is a two month amended.

Please search SEQ ID NO:1 in nucleic acid databases. Please search both SEQ ID NO:1 as well as the complement sequence. Please size limit the results to less than 50 bases (so that in the results only hits less than 50 bases will appear).

Thanks,
Melissa Schmidt
11d05
mailboxes 11e12

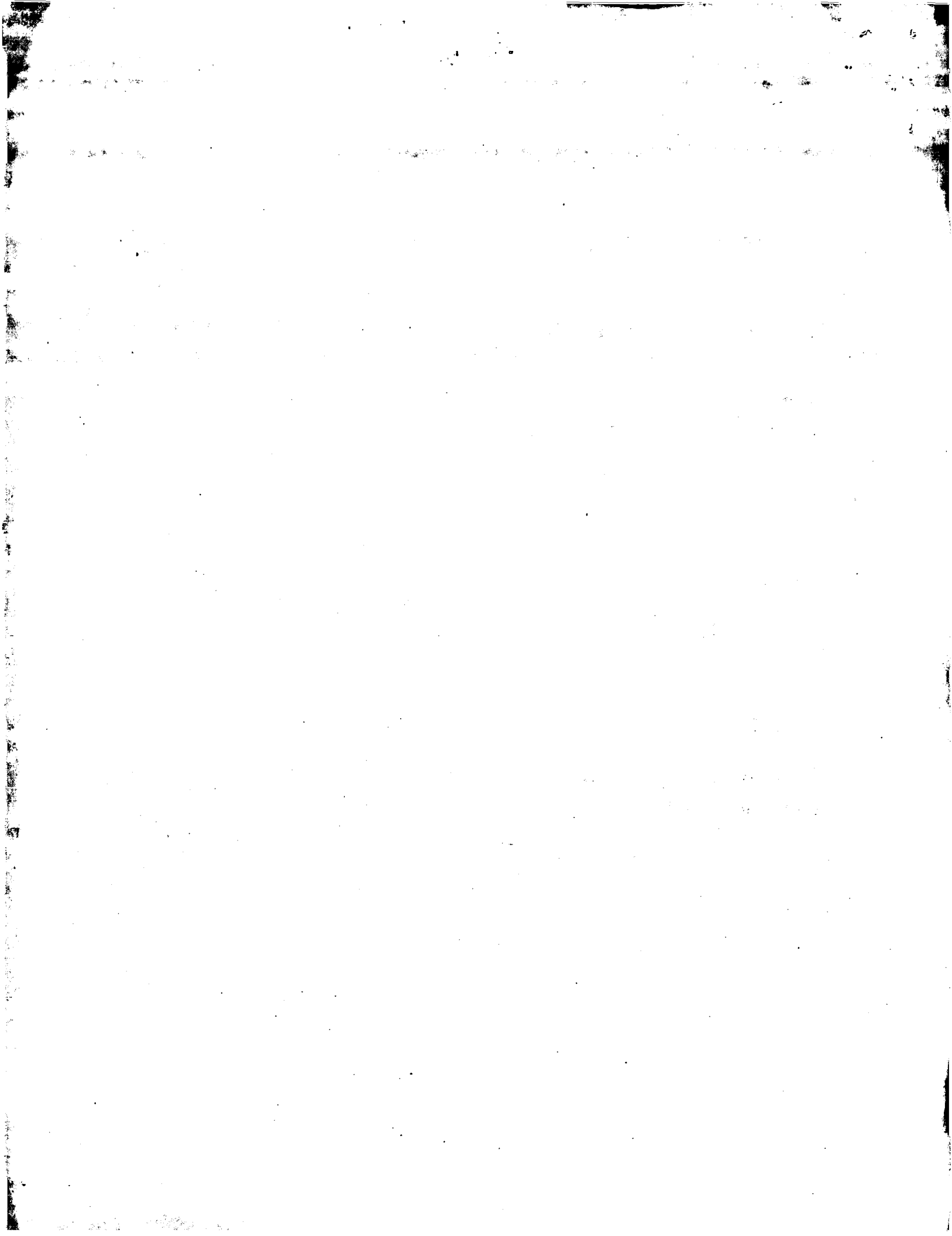
Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



au 1635
308-4471

96.021

Searcher: _____
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TYPE OF SEARCH:

NA Sequences: _____
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Bibliographic: _____
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Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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STAFF USE ONLY

Date completed: 06-16-03
Searcher: Beverly C4994
Terminal time: 21
Elapsed time: _____
CPU time: _____
Total time: 24
Number of Searches: _____
Number of Databases: 1

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other CGN

09/532001

FILE 'REGISTRY' ENTERED AT 09:51:15 ON 16 JUN 2003
L1 1 S CTGAGACCGATATCGGTCTCAG/SQSN

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS
RN 214357-65-0 REGISTRY
CN DNA, d(C-T-G-A-G-A-C-C-G-A-T-A-T-C-G-G-T-C-T-C-A-G) (9CI) (CA INDEX
NAME)
CI MAN
SQL 22

SEQ 1 ctgagaccga tatcgggtctc ag
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HITS AT: 1-22

REFERENCE 1: 129:301741

FILE 'HCAPLUS' ENTERED AT 09:52:34 ON 16 JUN 2003
L2 1 S L1

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:682556 HCAPLUS
DOCUMENT NUMBER: 129:301741
TITLE: Production of functional proteins: balance of
shear stress and gravity
INVENTOR(S): Goodwin, Thomas John; Hammond, Timothy Grant;
Kaysen, James Howard
PATENT ASSIGNEE(S): The United States of America as Represented by
the Administrator of the National Aeronautics
and Space Administration, USA; Administrators of
the Tulane Education Fund
SOURCE: PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9845468	A1	19981015	WO 1998-US6826	19980407
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
AU 9869534	A1	19981030	AU 1998-69534	19980407
EP 972069	A1	20000119	EP 1998-915320	19980407
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
BR 9808510	A	20000523	BR 1998-8510	19980407
JP 2001517081	T2	20011002	JP 1998-540983	19980407
PRIORITY APPLN. INFO.:			US 1997-43205P	P 19970408
			WO 1998-US6826	W 19980407
AB	The present invention provides a method for prodn. of functional			

09/532001

proteins, including hormones, by renal cells in a 3-dimensional co-culture process responsive to shear stress using a rotating wall vessel. Natural mixt. of renal cells expresses the enzyme 1.alpha.-hydroxylase, which can be used to generate the active form of vitamin D - 1,25-diOH vitamin D3. The fibroblast cultures and co-culture of renal cortical cells express the gene for erythropoietin and secrete erythropoietin into the culture supernatant. Other shear stress response genes are also modulated by shear stress, such as toxin receptors megalin and cubulin (gp280). Also provided is a method of treating in-need individual with the functional proteins produced in a 3-dimensional co-culture process responsive to shear stress using a rotating wall vessel.

IT 214357-65-0

RL: BUU (Biological use, unclassified); BIOL (Biological study);

USES (Uses)

(prodn. of functional proteins: balance of shear stress and gravity)

REFERENCE COUNT:

7

THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

FILE 'HOME' ENTERED AT 09:52:44 ON 16 JUN 2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 21:58:21 ; Search time 2130 Seconds
(without alignments)
259.688 Million cell updates/sec

Title: US-09-532-001-1

Perfect score: 22
Sequence: 1 CTGAGACCGATATCGTCTCAG 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

Pending_Patents_NA_Main:

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3	22	100.0	22	US-09-532-001-1	Sequence 1, Appli
4	22	100.0	22	US-09-532-001-1	Sequence 1, Appli
5	15.8	71.8	25	US-09-532-001-1	Sequence 245934
6	15.8	71.8	25	US-09-532-001-1	Sequence 245934
7	15.8	71.8	25	US-09-532-001-1	Sequence 245934
8	15.8	71.8	25	US-09-532-001-1	Sequence 245934
9	14.8	67.3	25	US-09-532-001-1	Sequence 201611
10	14.8	67.3	25	US-09-532-001-1	Sequence 201611
11	14.6	66.4	25	US-09-532-001-1	Sequence 403951
12	14.6	66.4	25	US-09-532-001-1	Sequence 371667
13	14.6	66.4	25	US-09-532-001-1	Sequence 18545
14	14.6	66.4	25	US-09-532-001-1	Sequence 18545
15	14.6	66.4	25	US-09-532-001-1	Sequence 371667
16	14.6	66.4	25	US-09-532-001-1	Sequence 371667
17	14.6	66.4	25	US-09-532-001-1	Sequence 20470
18	14.6	66.4	25	US-09-532-001-1	Sequence 20470
19	14.6	66.4	25	US-09-532-001-1	Sequence 99732
20	14.6	66.4	25	US-09-532-001-1	Sequence 99732
21	14.4	65.5	25	US-09-532-001-1	Sequence 216321

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	23	14.4	65.5	25	67	US-60-234-017-216691	Sequence 216691,	C	96	61.8	25	36	US-09-954-427-414182	Sequence 414182,
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C	25	14.2	64.5	25	79	US-60-353-987-90477	Sequence 90477, A	C	98	61.8	25	36	US-09-956-584-127968	Sequence 127968,
C	26	14.2	64.5	25	79	US-60-353-987-90477	Sequence 90477, A	C	99	61.8	25	67	US-60-233-166-41182	Sequence 41182,
C	27	14.2	64.5	28	1	US-09-959-10361-32	Sequence 32, App1	C	100	61.8	25	67	US-60-233-166-41182	Sequence 41182,
C	28	14.2	64.5	28	1	US-09-959-10361-32	Sequence 32, App1	C	101	61.8	25	67	US-60-233-620-48359	Sequence 48359, A
C	29	14.2	64.5	28	17	US-09-310-735-30	Sequence 30, App1	C	102	61.8	25	67	US-60-233-620-48359	Sequence 48359, A
C	30	14.2	64.5	28	17	US-09-310-735-30	Sequence 30, App1	C	103	61.8	25	67	US-60-234-017-82858	Sequence 82858, A
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C	33	14.2	64.5	28	17	US-09-310-735C-30	Sequence 30, App1	C	106	61.8	25	79	US-60-353-987-404087	Sequence 404087,
C	34	14.2	64.5	28	17	US-09-310-735C-30	Sequence 30, App1	C	107	61.8	25	79	US-60-353-987-700753	Sequence 700753,
C	35	14.2	64.5	28	17	US-09-310-761-30	Sequence 30, App1	C	108	61.8	25	79	US-60-353-987-700753	Sequence 700753,
C	36	14.2	64.5	28	17	US-09-310-761-30	Sequence 30, App1	C	109	61.8	25	79	US-60-353-987-829330	Sequence 829330,
C	37	14.2	64.5	28	17	US-09-310-762-30	Sequence 30, App1	C	110	61.8	25	79	US-60-353-987-829330	Sequence 829330,
C	38	14.2	64.5	28	17	US-09-310-762-30	Sequence 30, App1	C	111	61.8	31	18	US-09-655-684-164	Sequence 164, App
C	39	14.2	64.5	28	17	US-09-310-762A-30	Sequence 30, App1	C	112	61.8	25	36	US-09-954-427-261696	Sequence 261696,
C	40	14.2	64.5	28	17	US-09-310-762A-30	Sequence 30, App1	C	113	60.9	25	36	US-09-954-427-261696	Sequence 261696,
C	41	14.2	64.5	28	17	US-09-310-844-30	Sequence 30, App1	C	114	60.9	25	36	US-09-954-427-261696	Sequence 261696,
C	42	14.2	64.5	28	17	US-09-310-844-30	Sequence 30, App1	C	115	60.9	25	36	US-09-954-427-405466	Sequence 405466,
C	43	14.2	64.5	28	17	US-09-310-844B-30	Sequence 30, App1	C	116	60.9	25	36	US-09-954-427-405466	Sequence 405466,
C	44	14.2	64.5	28	17	US-09-310-844B-30	Sequence 30, App1	C	117	60.9	25	36	US-09-956-584-2699	Sequence 2699, App
C	45	14.2	64.5	28	17	US-09-310-844C-30	Sequence 30, App1	C	118	60.9	25	36	US-09-956-584-2699	Sequence 2699, App
C	46	14.2	64.5	28	17	US-09-310-844C-30	Sequence 30, App1	C	119	60.9	25	67	US-60-233-166-261696	Sequence 261696,
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C	48	14.2	64.5	28	17	US-09-310-907A-30	Sequence 30, App1	C	121	60.9	25	67	US-60-233-166-405466	Sequence 405466,
C	49	14.2	64.5	28	17	US-09-310-907C-30	Sequence 30, App1	C	122	60.9	25	67	US-60-233-166-405466	Sequence 405466,
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C	56	14	63.6	25	36	US-09-954-427-130199	Sequence 130199,	C	129	60.0	25	36	US-09-954-427-34972	Sequence 34972, A
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C	58	14	63.6	25	36	US-09-954-427-253994	Sequence 253994,	C	131	60.0	25	36	US-09-954-427-34972	Sequence 34972, A
C	59	14	63.6	25	67	US-60-233-166-130199	Sequence 130199,	C	132	60.0	25	36	US-09-954-427-43710	Sequence 43710, A
C	60	14	63.6	25	67	US-60-233-166-130199	Sequence 130199,	C	133	60.0	25	36	US-09-954-427-43710	Sequence 43710, A
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C	62	14	63.6	25	67	US-60-233-166-253994	Sequence 253994,	C	135	60.0	25	36	US-09-954-427-121920	Sequence 121920,
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C	67	14	63.6	25	79	US-60-353-987-576645	Sequence 576645,	C	140	60.0	25	36	US-09-954-427-253045	Sequence 253045,
C	68	14	63.6	25	79	US-60-353-987-802554	Sequence 802554,	C	141	60.0	25	36	US-09-954-427-253045	Sequence 253045,
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C	71	13.8	62.7	25	36	US-09-954-427-32867	Sequence 32867, A	C	144	60.0	25	36	US-09-954-427-223371	Sequence 223371,
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C	79	13.8	62.7	25	36	US-09-956-584-53197	Sequence 63197, A	C	152	60.0	25	36	US-09-956-604-112887	Sequence 132887,
C	80	13.8	62.7	25	36	US-09-956-584-53197	Sequence 63197, A	C	153	60.0	25	36	US-09-956-604-112887	Sequence 132887,
C	81	13.8	62.7	25	67	US-60-233-166-32867	Sequence 32867, A	C	154	60.0	25	36	US-09-956-604-112887	Sequence 132887,
C	82	13.8	62.7	25	67	US-60-233-166-32867	Sequence 32867, A	C	155	60.0	25	67	US-60-232-632-90122	Sequence 90122, A
C	83	13.8	62.7	25	67	US-60-233-166-253932	Sequence 253932,	C	156	60.0	25	67	US-60-232-632-90122	Sequence 90122, A
C	84	13.8	62.7	25	67	US-60-233-166-253932	Sequence 253932,	C	157	60.0	25	67	US-60-233-166-34972	Sequence 34972, A
C	85	13.8	62.7	25	67	US-60-233-166-253932	Sequence 253932,	C	158	60.0	25	67	US-60-233-166-34972	Sequence 34972, A
C	86	13.8	62.7	25	67	US-60-234-017-16155	Sequence 16155, A	C	159	60.0	25	67	US-60-233-166-43710	Sequence 43710, A
C	87	13.8	62.7	25	67	US-60-234-017-16155	Sequence 16155, A	C	160	60.0	25	67	US-60-233-166-43710	Sequence 43710, A
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C	89	13.8	62.7	25	67	US-60-234-017-11978	Sequence 31978, A	C	162	60.0	25	67	US-60-233-166-88029	Sequence 88029, A
C	90	13.8	62.7	25	67	US-60-234-017-11990	Sequence 31990, A	C	163	60.0	25	67	US-60-233-166-121920	Sequence 121920,
C	91	13.8	62.7	25	79	US-60-353-987-320105	Sequence 320105,	C	164	60.0	25	67	US-60-233-166-121920	Sequence 121920,
C	92	13.8	62.7	25	79	US-60-353-987-320105	Sequence 320105,	C	165	60.0	25	67	US-60-233-166-159861	Sequence 159861,
C	93	13.8	62.7	25	79	US-60-353-987-559692	Sequence 559692,	C	166	60.0	25	67	US-60-233-166-159861	Sequence 159861,
C	94	13.8	62.7	25	79	US-60-353-987-559692	Sequence 559692,	C	167	60.0	25	67	US-60-233-166-253045	Sequence 253045,

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C 169	13.2	60.0	25	67	US-60-233-166-385675	Sequence 385675,	C 242	13	59.1	25	67	US-60-233-017-1756	Sequence 1756, Ap
C 170	13.2	60.0	25	67	US-60-233-166-385675	Sequence 385675,	C 243	13	59.1	25	67	US-60-233-017-155659	Sequence 15565,
C 171	13.2	60.0	25	67	US-60-233-017-219112	Sequence 219112,	C 244	13	59.1	25	67	US-60-233-017-155659	Sequence 155659,
C 172	13.2	60.0	25	67	US-60-233-017-219112	Sequence 219112,	C 245	13	59.1	25	67	US-60-233-017-431329	Sequence 343129,
C 173	13.2	60.0	25	67	US-60-233-017-325329	Sequence 325329,	C 246	13	59.1	25	67	US-60-233-017-431329	Sequence 343129,
C 174	13.2	60.0	25	67	US-60-233-017-325329	Sequence 325329,	C 247	13	59.1	25	67	US-60-233-017-495976	Sequence 495976,
C 175	13.2	60.0	25	67	US-60-233-017-488667	Sequence 488667,	C 248	13	59.1	25	67	US-60-233-017-495976	Sequence 495976,
C 176	13.2	60.0	25	67	US-60-233-017-488667	Sequence 488667,	C 249	13	59.1	25	79	US-60-353-987-405911	Sequence 305911,
C 177	13.2	60.0	25	67	US-60-234-049-136309	Sequence 136309,	C 250	13	59.1	25	79	US-60-353-987-405911	Sequence 305911,
C 178	13.2	60.0	25	67	US-60-234-049-136309	Sequence 136309,	C 251	13	59.1	25	79	US-60-353-987-371036	Sequence 371036,
C 179	13.2	60.0	25	79	US-60-353-987-31235	Sequence 31235, A	C 252	13	59.1	25	79	US-60-353-987-371036	Sequence 371036,
C 180	13.2	60.0	25	79	US-60-353-987-31235	Sequence 31235, A	C 253	13	59.1	25	79	US-60-353-987-402225	Sequence 402225,
C 181	13.2	60.0	25	79	US-60-353-987-175333	Sequence 175333,	C 254	13	59.1	25	79	US-60-353-987-402225	Sequence 402225,
C 182	13.2	60.0	25	79	US-60-353-987-175333	Sequence 175333,	C 255	13	59.1	25	79	US-60-353-987-402225	Sequence 402225,
C 183	13.2	60.0	25	79	US-60-353-987-175334	Sequence 175334,	C 256	13	59.1	25	79	US-60-353-987-519794	Sequence 519794,
C 184	13.2	60.0	25	79	US-60-353-987-175334	Sequence 175334,	C 257	13	59.1	25	79	US-60-353-987-519794	Sequence 519794,
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C 187	13.2	60.0	25	79	US-60-353-987-403952	Sequence 403952,	C 260	13	59.1	25	79	US-60-353-987-797529	Sequence 797529,
C 188	13.2	60.0	25	79	US-60-353-987-417966	Sequence 417966,	C 261	13	59.1	25	79	US-60-353-987-797529	Sequence 797529,
C 189	13.2	60.0	25	79	US-60-353-987-417966	Sequence 417966,	C 262	13	59.1	25	79	US-60-353-987-797525	Sequence 875225,
C 190	13.2	60.0	25	79	US-60-353-987-453403	Sequence 453403,	C 263	13	59.1	25	79	US-60-353-987-797525	Sequence 875225,
C 191	13.2	60.0	25	79	US-60-353-987-657333	Sequence 657333,	C 264	13	59.1	25	79	US-60-353-987-657333	Sequence 657333,
C 192	13.2	60.0	25	79	US-60-353-987-657333	Sequence 657333,	C 265	13	59.1	25	79	US-60-353-987-657333	Sequence 657333,
C 193	13.2	60.0	25	79	US-60-353-987-701360	Sequence 701360,	C 266	13	59.1	25	79	US-60-353-987-701360	Sequence 701

C 314	12.8	58.2	25	36	US-09-956-584-93765	Sequence 93765, A	387	12.8	58.2	43	30	US-09-786-254-3	Sequence 3, Appli
C 315	12.8	58.2	25	36	US-09-956-584-93773	Sequence 93773, A	C 388	12.8	58.2	43	30	US-09-786-254-3	Sequence 3, Appli
C 316	12.8	58.2	25	36	US-09-956-584-93773	Sequence 93773, A	C 389	12.8	58.2	43	30	US-09-786-254-4	Sequence 4, Appli
C 317	12.8	58.2	25	36	US-09-956-584-231127	Sequence 231127, A	C 390	12.8	58.2	43	30	US-09-786-254-4	Sequence 4, Appli
C 318	12.8	58.2	25	36	US-09-956-584-231127	Sequence 231127, A	C 391	12.6	57.3	25	26	US-09-660-080-1605	Sequence 1605, Ap
C 319	12.8	58.2	25	36	US-09-956-584-242034	Sequence 242034, A	C 392	12.6	57.3	25	26	US-09-660-080-1605	Sequence 1605, Ap
C 320	12.8	58.2	25	36	US-09-956-584-242034	Sequence 242034, A	C 393	12.6	57.3	25	26	US-09-660-080-1606	Sequence 1606, Ap
C 321	12.8	58.2	25	36	US-09-956-584-264928	Sequence 264928, A	C 394	12.6	57.3	25	26	US-09-660-080-1606	Sequence 1606, Ap
C 322	12.8	58.2	25	36	US-09-956-584-264928	Sequence 264928, A	C 395	12.6	57.3	25	26	US-09-660-220-85019	Sequence 85019, A
C 323	12.8	58.2	25	36	US-09-956-604-69614	Sequence 69614, A	C 396	12.6	57.3	25	26	US-09-660-220-85019	Sequence 85019, A
C 324	12.8	58.2	25	36	US-09-956-604-69614	Sequence 69614, A	C 397	12.6	57.3	25	29	US-09-745-317-15	Sequence 15, Appli
C 325	12.8	58.2	25	36	US-09-956-604-128772	Sequence 128772, A	C 398	12.6	57.3	25	29	US-09-745-317-15	Sequence 15, Appli
C 326	12.8	58.2	25	36	US-09-956-604-128772	Sequence 128772, A	C 399	12.6	57.3	25	29	US-09-745-317A-15	Sequence 15, Appli
C 327	12.8	58.2	25	36	US-09-956-604A-69614	Sequence 69614, A	C 400	12.6	57.3	25	29	US-09-745-317A-15	Sequence 15, Appli
C 328	12.8	58.2	25	36	US-09-956-604A-69614	Sequence 69614, A	C 401	12.6	57.3	25	32	US-09-834-470-15	Sequence 15, Appli
C 329	12.8	58.2	25	36	US-09-956-604A-128772	Sequence 128772, A	C 402	12.6	57.3	25	32	US-09-834-470-15	Sequence 15, Appli
C 330	12.8	58.2	25	36	US-09-956-604A-128772	Sequence 128772, A	C 403	12.6	57.3	25	36	US-09-953-115-27469	Sequence 27469, A
C 331	12.8	58.2	25	36	US-09-956-604A-128772	Sequence 128772, A	C 404	12.6	57.3	25	36	US-09-953-115-27469	Sequence 27469, A
C 332	12.8	58.2	25	36	US-09-956-604B-69614	Sequence 69614, A	C 405	12.6	57.3	25	36	US-09-954-427-56630	Sequence 56630, A
C 333	12.8	58.2	25	36	US-09-956-604B-69614	Sequence 69614, A	C 406	12.6	57.3	25	36	US-09-954-427-56630	Sequence 56630, A
C 334	12.8	58.2	25	36	US-09-956-604B-128772	Sequence 128772, A	C 407	12.6	57.3	25	36	US-09-954-427-199323	Sequence 199323, A
C 335	12.8	58.2	25	67	US-60-233-166-29935	Sequence 29935, A	C 408	12.6	57.3	25	36	US-09-954-427-199323	Sequence 199323, A
C 336	12.8	58.2	25	67	US-60-233-166-29935	Sequence 29935, A	C 409	12.6	57.3	25	36	US-09-954-427-201932	Sequence 201932, A
C 337	12.8	58.2	25	67	US-60-233-166-321612	Sequence 321612, A	C 410	12.6	57.3	25	36	US-09-954-427-201932	Sequence 201932, A
C 338	12.8	58.2	25	67	US-60-233-166-321612	Sequence 321612, A	C 411	12.6	57.3	25	36	US-09-954-427-201946	Sequence 201946, A
C 339	12.8	58.2	25	67	US-60-233-166-372310	Sequence 372310, A	C 412	12.6	57.3	25	36	US-09-954-427-201946	Sequence 201946, A
C 340	12.8	58.2	25	67	US-60-233-166-372310	Sequence 372310, A	C 413	12.6	57.3	25	36	US-09-954-427-246324	Sequence 246324, A
C 341	12.8	58.2	25	67	US-60-233-166-372328	Sequence 372328, A	C 414	12.6	57.3	25	36	US-09-954-427-246324	Sequence 246324, A
C 342	12.8	58.2	25	67	US-60-233-166-372328	Sequence 372328, A	C 415	12.6	57.3	25	36	US-09-954-427-351292	Sequence 351292, A
C 343	12.8	58.2	25	67	US-60-233-166-372328	Sequence 372328, A	C 416	12.6	57.3	25	36	US-09-954-427-351292	Sequence 351292, A
C 344	12.8	58.2	25	67	US-60-233-166-414094	Sequence 414094, A	C 417	12.6	57.3	25	36	US-09-956-584-61206	Sequence 61206, A
C 345	12.8	58.2	25	67	US-60-233-166-414094	Sequence 414094, A	C 418	12.6	57.3	25	36	US-09-956-584-61206	Sequence 61206, A
C 346	12.8	58.2	25	67	US-60-233-620-119613	Sequence 119613, A	C 419	12.6	57.3	25	36	US-09-956-584-61207	Sequence 61207, A
C 347	12.8	58.2	25	67	US-60-233-620-119613	Sequence 119613, A	C 420	12.6	57.3	25	36	US-09-956-584-61207	Sequence 61207, A
C 348	12.8	58.2	25	67	US-60-233-620-130471	Sequence 130471, A	C 421	12.6	57.3	25	36	US-09-956-584-127973	Sequence 127973, A
C 349	12.8	58.2	25	67	US-60-234-017-13032	Sequence 13032, A	C 422	12.6	57.3	25	36	US-09-956-584-127973	Sequence 127973, A
C 350	12.8	58.2	25	67	US-60-234-017-13032	Sequence 13032, A	C 423	12.6	57.3	25	36	US-09-956-584-144179	Sequence 144179, A
C 351	12.8	58.2	25	67	US-60-234-017-13043	Sequence 13043, A	C 424	12.6	57.3	25	36	US-09-956-584-144179	Sequence 144179, A
C 352	12.8	58.2	25	67	US-60-234-017-13043	Sequence 13043, A	C 425	12.6	57.3	25	36	US-09-956-584-144181	Sequence 144181, A
C 353	12.8	58.2	25	67	US-60-234-017-113658	Sequence 113658, A	C 426	12.6	57.3	25	36	US-09-956-584-144181	Sequence 144181, A
C 354	12.8	58.2	25	67	US-60-234-017-113658	Sequence 113658, A	C 427	12.6	57.3	25	36	US-09-956-584-144189	Sequence 144189, A
C 355	12.8	58.2	25	67	US-60-234-017-113658	Sequence 113658, A	C 428	12.6	57.3	25	36	US-09-956-584-144189	Sequence 144189, A
C 356	12.8	58.2	25	67	US-60-234-017-113658	Sequence 113658, A	C 429	12.6	57.3	25	36	US-09-956-584-144189	Sequence 144189, A
C 357	12.8	58.2	25	67	US-60-234-017-216390	Sequence 216390, A	C 430	12.6	57.3	25	36	US-09-956-584-203851	Sequence 203851, A
C 358	12.8	58.2	25	67	US-60-234-017-216390	Sequence 216390, A	C 431	12.6	57.3	25	36	US-09-956-584-380813	Sequence 380813, A
C 359	12.8	58.2	25	67	US-60-234-017-243858	Sequence 243858, A	C 432	12.6	57.3	25	36	US-09-956-584-380813	Sequence 380813, A
C 360	12.8	58.2	25	67	US-60-234-017-243858	Sequence 243858, A	C 433	12.6	57.3	25	36	US-09-956-584-518772	Sequence 518772, A
C 361	12.8	58.2	25	67	US-60-234-017-296877	Sequence 296877, A	C 434	12.6	57.3	25	36	US-09-956-584-518772	Sequence 518772, A
C 362	12.8	58.2	25	67	US-60-234-017-296877	Sequence 296877, A	C 435	12.6	57.3	25	36	US-09-956-584-593770	Sequence 593770, A
C 363	12.8	58.2	25	67	US-60-234-049-76342	Sequence 76342, A	C 436	12.6	57.3	25	36	US-09-956-604-22675	Sequence 22675, A
C 364	12.8	58.2	25	67	US-60-234-049-76342	Sequence 76342, A	C 437	12.6	57.3	25	36	US-09-956-604-22675	Sequence 22675, A
C 365	12.8	58.2	25	67	US-60-234-049-94045	Sequence 94045, A	C 438	12.6	57.3	25	36	US-09-956-604-22675	Sequence 22675, A
C 366	12.8	58.2	25	67	US-60-234-049-94045	Sequence 94045, A	C 439	12.6	57.3	25	36	US-09-956-604A-22675	Sequence 22675, A
C 367	12.8	58.2	25	67	US-60-234-049-94045	Sequence 94045, A	C 440	12.6	57.3	25	36	US-09-956-604A-22675	Sequence 22675, A
C 368	12.8	58.2	25	67	US-60-353-987-75051	Sequence 75051, A	C 441	12.6	57.3	25	36	US-09-956-604B-22675	Sequence 22675, A
C 369	12.8	58.2	25	67	US-60-353-987-75051	Sequence 75051, A	C 442	12.6	57.3	25	36	US-09-956-604B-22675	Sequence 22675, A
C 370	12.8	58.2	25	67	US-60-353-987-509664	Sequence 509664, A	C 443	12.6	57.3	25	41	US-10-170-332-15	Sequence 15, Appli
C 371	12.8	58.2	25	67	US-60-353-987-788258	Sequence 788258, A	C 444	12.6	57.3	25	41	US-10-170-332-15	Sequence 15, Appli
C 372	12.8	58.2	25	67	US-60-353-987-788258	Sequence 788258, A	C 445	12.6	57.3	25	67	US-60-233-166-56630	Sequence 56630, A
C 373	12.8	58.2	25	67	US-60-353-987-788258	Sequence 788258, A	C 446	12.6	57.3	25	67	US-60-233-166-56630	Sequence 56630, A
C 374	12.8	58.2	25	67	US-60-353-987-940701	Sequence 940701, A	C 447	12.6	57.3	25	67	US-60-233-166-199323	Sequence 199323, A
C 375	12.8	58.2	25	67	US-60-353-987-940701	Sequence 940701, A	C 448	12.6	57.3	25	67	US-60-233-166-199323	Sequence 199323, A
C 376	12.8	58.2	25	67	US-60-233-166-201932	Sequence 201932, A	C 449	12.6	57.3	25	67	US-60-233-166-201932	Sequence 201932, A
C 377	12.8	58.2	25	67	US-60-233-166-201932	Sequence 201932, A	C 450	12.6	57.3	25	67	US-60-233-166-201932	Sequence 201932, A
C 378	12.8	58.2	25	67	US-60-233-166-201946	Sequence 201946, A	C 451	12.6	57.3	25	67	US-60-233-166-201946	Sequence 201946, A
C 379	12.8	58.2	25	67	US-60-233-166-201946	Sequence 201946, A	C 452	12.6	57.3	25	67	US-60-233-166-201946	Sequence 201946, A
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C 381	12.8	58.2	25	67	US-60-233-166-246324	Sequence 246324, A	C 454	12.6	57.3	25	67	US-60-233-166-246324	Sequence 246324, A
C 382	12.8	58.2	25	67	US-60-233-166-351292	Sequence 351292, A	C 455	12.6	57.3	25	67	US-60-233-166-351292	Sequence 351292, A
C 383	12.8	58.2	25	67	US-60-233-166-351292	Sequence 351292, A	C 456	12.6	57.3	25	67	US-60-233-166-351292	Sequence 351292, A
C 384	12.8	58.2	25	67	US-60-233-620-33743	Sequence 33743, A	C 457	12.6	57.3	25	67	US-60-233-620-33743	Sequence 33743, A
C 385	12.8	58.2	25	67	US-60-233-620-33743	Sequence 33743, A	C 458	12.6	57.3	25	67	US-60-233-620-33743	Sequence 33743, A
C 386	12.8	58.2	43	1	US-60-233-620-33744	Sequence 33744, A	C 459	12.6	57.3	25	67	US-60-233-620-33744	Sequence 33744, A

C 460	12.6	57.3	25	67	US-60-233-620-33744	Sequence 33744, A	533	12.4	56.4	25	26	US-09-660-220-114462	Sequence 114462,
C 461	12.6	57.3	25	67	US-60-233-620-99983	Sequence 99983, A	534	12.4	56.4	25	26	US-09-660-220-114462	Sequence 114462,
C 462	12.6	57.3	25	67	US-60-233-620-99983	Sequence 99983, A	535	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 463	12.6	57.3	25	67	US-60-233-620-128690	Sequence 128690,	536	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 464	12.6	57.3	25	67	US-60-233-620-128690	Sequence 128690,	537	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 465	12.6	57.3	25	67	US-60-233-620-128691	Sequence 128691,	538	12.4	56.4	25	26	US-09-660-220-139083	Sequence 139083,
C 466	12.6	57.3	25	67	US-60-233-620-128691	Sequence 128691,	539	12.4	56.4	25	26	US-09-660-220-139083	Sequence 139083,
C 467	12.6	57.3	25	67	US-60-234-017-23057	Sequence 23057, A	540	12.4	56.4	25	36	US-09-953-1115-11189	Sequence 11189, A
C 468	12.6	57.3	25	67	US-60-234-017-23058	Sequence 23058, A	541	12.4	56.4	25	36	US-09-953-1115-11189	Sequence 11189, A
C 469	12.6	57.3	25	67	US-60-234-017-23058	Sequence 23058, A	542	12.4	56.4	25	36	US-09-954-427-121041	Sequence 121041,
C 470	12.6	57.3	25	67	US-60-234-017-23058	Sequence 23058, A	543	12.4	56.4	25	36	US-09-954-427-121041	Sequence 121041,
C 471	12.6	57.3	25	67	US-60-234-017-82848	Sequence 82848, A	544	12.4	56.4	25	36	US-09-954-427-124080	Sequence 124080,
C 472	12.6	57.3	25	67	US-60-234-017-82848	Sequence 82848, A	545	12.4	56.4	25	36	US-09-954-427-131755	Sequence 131755,
C 473	12.6	57.3	25	67	US-60-234-017-161860	Sequence 161860,	546	12.4	56.4	25	36	US-09-954-427-131755	Sequence 131755,
C 474	12.6	57.3	25	67	US-60-234-017-161860	Sequence 161860,	547	12.4	56.4	25	36	US-09-954-427-203323	Sequence 203323,
C 475	12.6	57.3	25	67	US-60-234-017-161866	Sequence 161866,	548	12.4	56.4	25	36	US-09-954-427-203323	Sequence 203323,
C 476	12.6	57.3	25	67	US-60-234-017-161866	Sequence 161866,	549	12.4	56.4	25	36	US-09-954-427-203525	Sequence 203525,
C 477	12.6	57.3	25	67	US-60-234-017-161872	Sequence 161872,	550	12.4	56.4	25	36	US-09-954-427-23525	Sequence 23525,
C 478	12.6	57.3	25	67	US-60-234-017-161872	Sequence 161872,	551	12.4	56.4	25	36	US-09-954-427-23525	Sequence 23525,
C 479	12.6	57.3	25	67	US-60-234-017-161872	Sequence 161872,	552	12.4	56.4	25	36	US-09-954-427-415703	Sequence 415703,
C 480	12.6	57.3	25	67	US-60-234-017-205345	Sequence 205345,	553	12.4	56.4	25	36	US-09-954-427-415703	Sequence 415703,
C 481	12.6	57.3	25	67	US-60-234-017-364215	Sequence 364215,	554	12.4	56.4	25	36	US-09-956-584-12701	Sequence 12701, Ap
C 482	12.6	57.3	25	67	US-60-234-017-364215	Sequence 364215,	555	12.4	56.4	25	36	US-09-956-584-39363	Sequence 39363, A
C 483	12.6	57.3	25	67	US-60-234-017-486871	Sequence 486871,	556	12.4	56.4	25	36	US-09-956-584-39363	Sequence 39363, A
C 484	12.6	57.3	25	67	US-60-234-017-486871	Sequence 486871,	557	12.4	56.4	25	36	US-09-956-584-63348	Sequence 63348, A
C 485	12.6	57.3	25	67	US-60-234-017-604091	Sequence 604091,	558	12.4	56.4	25	36	US-09-956-584-63348	Sequence 63348, A
C 486	12.6	57.3	25	67	US-60-234-017-604091	Sequence 604091,	559	12.4	56.4	25	36	US-09-956-584-63348	Sequence 63348, A
C 487	12.6	57.3	25	67	US-60-234-017-604091	Sequence 604091,	560	12.4	56.4	25	36	US-09-956-584-66217	Sequence 66217, A
C 488	12.6	57.3	25	67	US-60-234-049-56620	Sequence 56620, A	561	12.4	56.4	25	36	US-09-956-584-66217	Sequence 66217, A
C 489	12.6	57.3	25	67	US-60-234-049-56620	Sequence 56620, A	562	12.4	56.4	25	36	US-09-956-584-88938	Sequence 88938, A
C 490	12.6	57.3	25	79	US-60-333-987-5941	Sequence 5941, Ap	563	12.4	56.4	25	36	US-09-956-584-88938	Sequence 88938, A
C 491	12.6	57.3	25	79	US-60-333-987-5941	Sequence 5941, Ap	564	12.4	56.4	25	36	US-09-956-584-88940	Sequence 88940, A
C 492	12.6	57.3	25	79	US-60-333-987-5942	Sequence 5942, Ap	565	12.4	56.4	25	36	US-09-956-584-88940	Sequence 88940, A
C 493	12.6	57.3	25	79	US-60-333-987-5942	Sequence 5942, Ap	566	12.4	56.4	25	36	US-09-956-584-93774	Sequence 93774, A
C 494	12.6	57.3	25	79	US-60-333-987-90478	Sequence 90478, A	567	12.4	56.4	25	36	US-09-956-584-93774	Sequence 93774, A
C 495	12.6	57.3	25	79	US-60-333-987-90478	Sequence 90478, A	568	12.4	56.4	25	36	US-09-956-584-109529	Sequence 109529,
C 496	12.6	57.3	25	79	US-60-333-987-283495	Sequence 283495,	569	12.4	56.4	25	36	US-09-956-584-109529	Sequence 109529,
C 497	12.6	57.3	25	79	US-60-333-987-283495	Sequence 283495,	570	12.4	56.4	25	36	US-09-956-584-131800	Sequence 131800,
C 498	12.6	57.3	25	79	US-60-333-987-297457	Sequence 297457,	571	12.4	56.4	25	36	US-09-956-584-131800	Sequence 131800,
C 499	12.6	57.3	25	79	US-60-333-987-297457	Sequence 297457,	572	12.4	56.4	25	36	US-09-956-584-136425	Sequence 136425,
C 500	12.6	57.3	25	79	US-60-333-987-337874	Sequence 337874,	573	12.4	56.4	25	36	US-09-956-584-136425	Sequence 136425,
C 501	12.6	57.3	25	79	US-60-333-987-337874	Sequence 337874,	574	12.4	56.4	25	36	US-09-956-584-207883	Sequence 207883,
C 502	12.6	57.3	25	79	US-60-333-987-540297	Sequence 540297,	575	12.4	56.4	25	36	US-09-956-584-207883	Sequence 207883,
C 503	12.6	57.3	25	79	US-60-333-987-540297	Sequence 540297,	576	12.4	56.4	25	36	US-09-956-584-226472	Sequence 226472,
C 504	12.6	57.3	25	79	US-60-333-987-564953	Sequence 564953,	577	12.4	56.4	25	36	US-09-956-584-226472	Sequence 226472,
C 505	12.6	57.3	25	79	US-60-333-987-564953	Sequence 564953,	578	12.4	56.4	25	36	US-09-956-584-226473	Sequence 226473,
C 506	12.6	57.3	25	79	US-60-333-987-639291	Sequence 639291,	579	12.4	56.4	25	36	US-09-956-584-226473	Sequence 226473,
C 507	12.6	57.3	25	79	US-60-333-987-639291	Sequence 639291,	580	12.4	56.4	25	36	US-09-956-584-226474	Sequence 226474,
C 508	12.6	57.3	25	79	US-60-333-987-735589	Sequence 735589,	581	12.4	56.4	25	36	US-09-956-584-226474	Sequence 226474,
C 509	12.6	57.3	25	79	US-60-333-987-735589	Sequence 735589,	582	12.4	56.4	25	36	US-09-956-584-295609	Sequence 295609,
C 510	12.6	57.3	25	79	US-60-333-987-887212	Sequence 887212,	583	12.4	56.4	25	36	US-09-956-584-340514	Sequence 340514,
C 511	12.6	57.3	25	79	US-60-333-987-887212	Sequence 887212,	584	12.4	56.4	25	36	US-09-956-584-340514	Sequence 340514,
C 512	12.6	57.3	25	79	US-60-333-987-898442	Sequence 898442,	585	12.4	56.4	25	36	US-09-956-584-392203	Sequence 392203,
C 513	12.6	57.3	25	79	US-60-333-987-898442	Sequence 898442,	586	12.4	56.4	25	36	US-09-956-584-392203	Sequence 392203,
C 514	12.6	57.3	25	79	US-60-333-987-899706	Sequence 899706,	587	12.4	56.4	25	36	US-09-956-584-418163	Sequence 418163,
C 515	12.6	57.3	25	79	US-60-333-987-899706	Sequence 899706,	588	12.4	56.4	25	36	US-09-956-584-418163	Sequence 418163,
C 516	12.6	57.3	25	79	PCT-US01-47856-2060	Sequence 2060, Ap	589	12.4	56.4	25	36	US-09-956-584-418171	Sequence 418171,
C 517	12.6	57.3	25	79	PCT-US01-47856-2060	Sequence 2060, Ap	590	12.4	56.4	25	36	US-09-956-584-418171	Sequence 418171,
C 518	12.6	57.3	25	79	US-10-131-827-2060	Sequence 2060, Ap	591	12.4	56.4	25	36	US-09-956-584-418171	Sequence 418171,
C 519	12.6	57.3	25	79	US-10-131-827-2060	Sequence 2060, Ap	592	12.4	56.4	25	36	US-09-956-604-86954	Sequence 86954, A
C 520	12.6	57.3	25	79	US-10-131-831-2060	Sequence 2060, Ap	593	12.4	56.4	25	36	US-09-956-604-86954	Sequence 86954, A
C 521	12.6	57.3	25	79	US-10-131-831-2060	Sequence 2060, Ap	594	12.4	56.4	25	36	US-09-956-604-86957	Sequence 86957, A
C 522	12.6	57.3	25	79	US-09-201-228A-5711	Sequence 5711, Ap	595	12.4	56.4	25	36	US-09-956-604-86957	Sequence 86957, A
C 523	12.6	57.3	25	79	US-09-201-228A-5711	Sequence 5711, Ap	596	12.4	56.4	25	36	US-09-956-604-86990	Sequence 86990, A
C 524	12.6	57.3	25	79	US-09-284-725-33	Sequence 33, Appl	597	12.4	56.4	25	36	US-09-956-604-86990	Sequence 86990, A
C 525	12.6	57.3	25	79	US-09-284-725-33	Sequence 33, Appl	598	12.4	56.4	25	36	US-09-956-604A-86954	Sequence 86954, A
C 526	12.6	57.3	25	79	US-10-263-594-33	Sequence 33, Appl	599	12.4	56.4	25	36	US-09-956-604A-86957	Sequence 86957, A
C 527	12.6	57.3	25	79	US-10-263-594-33	Sequence 33, Appl	600	12.4	56.4	25	36	US-09-956-604A-86957	Sequence 86957, A
C 528	12.6	57.3	25	79	US-09-660-080-10272	Sequence 10272, A	601	12.4	56.4	25	36	US-09-956-604A-86957	Sequence 86957, A
C 529	12.6	57.3	25	79	US-09-660-080-10272	Sequence 10272, A	602	12.4	56.4	25	36	US-09-956-604A-86990	Sequence 86990, A
C 530	12.6	57.3	25	79	US-09-660-080-10272	Sequence 10272, A	603	12.4	56.4	25	36	US-09-956-604A-86990	Sequence 86990, A
C 531	12.4	56.4	25	26	US-09-660-220-62449	Sequence 62449, A	604	12.4	56.4	25	36	US-09-956-604B-86954	Sequence 86954, A
C 532	12.4	56.4	25	26	US-09-660-220-62455	Sequence 62455, A	605	12.4	56.4	25	36	US-09-956-604B-86957	Sequence 86957, A
C 533	12.4	56.4	25	26	US-09-660-220-62455	Sequence 62455, A	606	12.4	56.4	25	36	US-09-956-604B-86957	Sequence 86957, A

C 606	12.4	56.4	25	36	US-09-956-604B-86937	Sequence	86957, A	679	12.4	56.4	25	79	US-60-355-987-387487	Sequen
C 607	12.4	56.4	25	36	US-09-956-604B-86930	Sequence	86990, A	C 680	12.4	56.4	25	79	US-60-355-987-387487	Sequen
C 608	12.4	56.4	25	36	US-09-956-604B-86930	Sequence	86990, A	C 681	12.4	56.4	25	79	US-60-355-987-399725	Sequen
C 609	12.4	56.4	25	67	US-60-233-638-137844	Sequence	137844, A	C 682	12.4	56.4	25	79	US-60-355-987-399725	Sequen
C 610	12.4	56.4	25	67	US-60-233-638-137844	Sequence	137844, A	C 683	12.4	56.4	25	79	US-60-355-987-440638	Sequen
C 611	12.4	56.4	25	67	US-60-233-166-121041	Sequence	121041, A	C 684	12.4	56.4	25	79	US-60-355-987-440638	Sequen
C 612	12.4	56.4	25	67	US-60-233-166-121041	Sequence	121041, A	C 685	12.4	56.4	25	79	US-60-355-987-47473	Sequen
C 613	12.4	56.4	25	67	US-60-233-166-124080	Sequence	124080, A	C 686	12.4	56.4	25	79	US-60-355-987-47473	Sequen
C 614	12.4	56.4	25	67	US-60-233-166-124080	Sequence	124080, A	C 687	12.4	56.4	25	79	US-60-355-987-475721	Sequen
C 615	12.4	56.4	25	67	US-60-233-166-11755	Sequence	11755, A	C 688	12.4	56.4	25	79	US-60-355-987-475721	Sequen
C 616	12.4	56.4	25	67	US-60-233-166-131755	Sequence	131755, A	C 689	12.4	56.4	25	79	US-60-355-987-475722	Sequen
C 617	12.4	56.4	25	67	US-60-233-166-203323	Sequence	203323, A	C 690	12.4	56.4	25	79	US-60-355-987-475722	Sequen
C 618	12.4	56.4	25	67	US-60-233-166-203323	Sequence	203323, A	C 691	12.4	56.4	25	79	US-60-355-987-482340	Sequen
C 619	12.4	56.4	25	67	US-60-233-166-239525	Sequence	239525, A	C 692	12.4	56.4	25	79	US-60-355-987-482340	Sequen
C 620	12.4	56.4	25	67	US-60-233-166-239525	Sequence	239525, A	C 693	12.4	56.4	25	79	US-60-355-987-576637	Sequen
C 621	12.4	56.4	25	67	US-60-233-166-415703	Sequence	415703, A	C 694	12.4	56.4	25	79	US-60-355-987-576637	Sequen
C 622	12.4	56.4	25	67	US-60-233-166-415703	Sequence	415703, A	C 695	12.4	56.4	25	79	US-60-355-987-576646	Sequen
C 623	12.4	56.4	25	67	US-60-233-620-11503	Sequence	11503, A	C 696	12.4	56.4	25	79	US-60-355-987-576646	Sequen
C 624	12.4	56.4	25	67	US-60-233-620-11503	Sequence	11503, A	C 697	12.4	56.4	25	79	US-60-355-987-579566	Sequen
C 625	12.4	56.4	25	67	US-60-233-017-14542	Sequence	14542, A	C 698	12.4	56.4	25	79	US-60-355-987-579566	Sequen
C 626	12.4	56.4	25	67	US-60-233-017-14542	Sequence	14542, A	C 699	12.4	56.4	25	79	US-60-355-987-608149	Sequen
C 627	12.4	56.4	25	67	US-60-233-017-27012	Sequence	27012, A	C 700	12.4	56.4	25	79	US-60-355-987-608149	Sequen
C 628	12.4	56.4	25	67	US-60-233-017-27012	Sequence	27012, A	C 701	12.4	56.4	25	79	US-60-355-987-626708	Sequen
C 629	12.4	56.4	25	67	US-60-233-017-31988	Sequence	31988, A	C 702	12.4	56.4	25	79	US-60-355-987-626708	Sequen
C 630	12.4	56.4	25	67	US-60-233-017-31988	Sequence	31988, A	C 703	12.4	56.4	25	79	US-60-355-987-80253	Sequen
C 631	12.4	56.4	25	67	US-60-233-017-105486	Sequence	105486, A	C 704	12.4	56.4	25	79	US-60-355-987-80253	Sequen
C 632	12.4	56.4	25	67	US-60-233-017-105486	Sequence	105486, A	C 705	12.4	56.4	25	79	US-60-355-987-814469	Sequen
C 633	12.4	56.4	25	67	US-60-233-017-113671	Sequence	113671, A	C 706	12.4	56.4	25	79	US-60-355-987-814469	Sequen
C 634	12.4	56.4	25	67	US-60-233-017-113671	Sequence	113671, A	C 707	12.4	56.4	25	79	US-60-355-987-814470	Sequen
C 635	12.4	56.4	25	67	US-60-233-017-117796	Sequence	117796, A	C 708	12.4	56.4	25	79	US-60-355-987-814470	Sequen
C 636	12.4	56.4	25	67	US-60-233-017-117796	Sequence	117796, A	C 709	12.4	56.4	25	79	US-60-355-987-825522	Sequen
C 637	12.4	56.4	25	67	US-60-233-017-119650	Sequence	119650, A	C 710	12.4	56.4	25	79	US-60-355-987-825522	Sequen
C 638	12.4	56.4	25	67	US-60-233-017-119650	Sequence	119650, A	C 711	12.4	56.4	25	79	US-60-355-987-923571	Sequen
C 639	12.4	56.4	25	67	US-60-233-017-119655	Sequence	119655, A	C 712	12.4	56.4	25	79	US-60-355-987-923571	Sequen
C 640	12.4	56.4	25	67	US-60-233-017-119655	Sequence	119655, A	C 713	12.4	56.4	25	79	US-60-355-987-954030	Sequen
C 641	12.4	56.4	25	67	US-60-233-017-133988	Sequence	133988, A	C 714	12.4	56.4	25	79	US-60-355-987-954030	Sequen
C 642	12.4	56.4	25	67	US-60-233-017-133988	Sequence	133988, A	C 715	12.4	56.4	32	6	US-08-257-663-22	Sequen
C 643	12.4	56.4	25	67	US-60-233-017-163089	Sequence	163089, A	C 716	12.4	56.4	32	6	US-08-257-663-22	Sequen
C 644	12.4	56.4	25	67	US-60-233-017-163089	Sequence	163089, A	C 717	12.4	56.4	32	6	US-08-257-663-22	Sequen
C 645	12.4	56.4	25	67	US-60-233-017-212846	Sequence	212846, A	C 718	12.4	56.4	32	6	US-08-257-663-22	Sequen
C 646	12.4	56.4	25	67	US-60-233-017-212846	Sequence	212846, A	C 719	12.4	56.4	39	18	US-09-404-520-39928	Sequen
C 647	12.4	56.4	25	67	US-60-233-017-226059	Sequence	226059, A	C 720	12.4	56.4	39	18	US-09-404-520-39928	Sequen
C 648	12.4	56.4	25	67	US-60-233-017-226059	Sequence	226059, A	C 721	12.4	56.4	39	79	US-60-355-987-3362	Sequen
C 649	12.4	56.4	25	67	US-60-233-017-226067	Sequence	226067, A	C 722	12.4	56.4	39	79	US-60-355-987-3362	Sequen
C 650	12.4	56.4	25	67	US-60-233-017-226067	Sequence	226067, A	C 723	12.4	56.4	40	18	US-09-404-520-37306	Sequen
C 651	12.4	56.4	25	67	US-60-233-017-226068	Sequence	226068, A	C 724	12.4	56.4	40	18	US-09-404-520-37306	Sequen
C 652	12.4	56.4	25	67	US-60-233-017-226068	Sequence	226068, A	C 725	12.4	56.4	43	18	US-09-404-520-34586	Sequen
C 653	12.4	56.4	25	67	US-60-233-017-312039	Sequence	312039, A	C 726	12.4	56.4	43	18	US-09-404-520-34586	Sequen
C 654	12.4	56.4	25	67	US-60-233-017-312039	Sequence	312039, A	C 727	12.4	56.4	44	18	US-09-404-520-34586	Sequen
C 655	12.4	56.4	25	67	US-60-233-017-312522	Sequence	312522, A	C 728	12.4	56.4	44	18	US-09-404-520-34586	Sequen
C 656	12.4	56.4	25	67	US-60-233-017-312522	Sequence	312522, A	C 729	12.4	56.4	49	69	US-60-255-654-10686	Sequen
C 657	12.4	56.4	25	67	US-60-233-017-446610	Sequence	446610, A	C 730	12.4	56.4	49	69	US-60-255-654-10686	Sequen
C 658	12.4	56.4	25	67	US-60-233-017-446610	Sequence	446610, A	C 731	12.4	56.4	49	69	US-60-255-654-10686	Sequen
C 659	12.4	56.4	25	67	US-60-233-017-453458	Sequence	453458, A	C 732	12.4	56.4	49	69	US-60-255-654-10686	Sequen
C 660	12.4	56.4	25	67	US-60-233-017-453458	Sequence	453458, A	C 733	12.4	56.4	49	69	US-60-255-654-10686	Sequen
C 661	12.4	56.4	25	67	US-60-233-017-453465	Sequence	453465, A	C 734	12.2	55.5	24	17	US-09-309-038-12	Sequen
C 662	12.4	56.4	25	67	US-60-233-017-453465	Sequence	453465, A	C 735	12.2	55.5	25	26	US-09-660-220-33414	Sequen
C 663	12.4	56.4	25	67	US-60-233-049-108820	Sequence	108820, A	C 736	12.2	55.5	25	26	US-09-660-220-33414	Sequen
C 664	12.4	56.4	25	67	US-60-233-049-108820	Sequence	108820, A	C 737	12.2	55.5	25	26	US-09-660-220-81573	Sequen
C 665	12.4	56.4	25	67	US-60-233-049-108831	Sequence	108831, A	C 738	12.2	55.5	25	26	US-09-660-220-81573	Sequen
C 666	12.4	56.4	25	67	US-60-233-049-108831	Sequence	108831, A	C 739	12.2	55.5	25	26	US-09-660-220-81573	Sequen
C 667	12.4	56.4	25	67	US-60-233-049-108843	Sequence	108843, A	C 740	12.2	55.5	25	36	US-09-954-427-11636	Sequen
C 668	12.4	56.4	25	67	US-60-233-049-108843	Sequence	108843, A	C 741	12.2	55.5	25	36	US-09-954-427-11636	Sequen
C 669	12.4	56.4	25	79	US-60-355-987-84972	Sequence	84972, A	C 742	12.2	55.5	25	36	US-09-954-427-115732	Sequen
C 670	12.4	56.4	25	79	US-60-355-987-84972	Sequence	84972, A	C 743	12.2	55.5	25	36	US-09-954-427-115732	Sequen
C 671	12.4	56.4	25	79	US-60-355-987-84972	Sequence	84972, A	C 744	12.2	55.5	25	36	US-09-954-427-115732	Sequen
C 672	12.4	56.4	25	79	US-60-355-987-167123	Sequence	167123, A	C 745	12.2	55.5	25	36	US-09-954-427-115732	Sequen
C 673	12.4	56.4	25	79	US-60-355-987-167123	Sequence	167123, A	C 746	12.2	55.5	25	36	US-09-954-427-118837	Sequen
C 674	12.4	56.4	25	79	US-60-355-987-194918	Sequence	194918, A	C 747	12.2	55.5	25	36	US-09-954-427-118837	Sequen
C 675	12.4	56.4	25	79	US-60-355-987-194918	Sequence	194918, A	C 748	12.2	55.5	25	36	US-09-954-427-118824	Sequen
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C 677	12.4	56.4	25	79	US-60-355-987-316226	Sequence	316226, A	C 750	12.2	55.5	25	36	US-09-954-427-195631	Sequen
C 678	12.4	56.4	25	79	US-60-355-987-319261	Sequence	319261, A	C 751	12.2	55.5	25	36	US-09-954-427-310397	Sequen

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C 754	12.2	55.5	25	36	US-09-954-427-210470	Sequence 210470,	827	12.2	55.5	25	36	US-09-956-604A-15919	Sequence 15919, A
C 755	12.2	55.5	25	36	US-09-954-427-236403	Sequence 236403,	C 828	12.2	55.5	25	36	US-09-956-604A-15919	Sequence 15919, A
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C 757	12.2	55.5	25	36	US-09-954-427-248159	Sequence 248159,	C 830	12.2	55.5	25	36	US-09-956-604A-18099	Sequence 18099, A
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C 766	12.2	55.5	25	36	US-09-954-427-284273	Sequence 284273,	839	12.2	55.5	25	67	US-60-232-638-76421	Sequence 76421, A
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C 770	12.2	55.5	25	36	US-09-954-427-297318	Sequence 297318,	843	12.2	55.5	25	67	US-60-233-166-115732	Sequence 115732,
C 771	12.2	55.5	25	36	US-09-954-427-300068	Sequence 300068,	C 844	12.2	55.5	25	67	US-60-233-166-115732	Sequence 115732,
C 772	12.2	55.5	25	36	US-09-954-427-300068	Sequence 300068,	845	12.2	55.5	25	67	US-60-233-166-115743	Sequence 115743,
C 773	12.2	55.5	25	36	US-09-954-427-360973	Sequence 360973,	C 846	12.2	55.5	25	67	US-60-233-166-115743	Sequence 115743,
C 774	12.2	55.5	25	36	US-09-954-427-360973	Sequence 360973,	847	12.2	55.5	25	67	US-60-233-166-118837	Sequence 118837,
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C 776	12.2	55.5	25	36	US-09-954-427-391130	Sequence 391130,	849	12.2	55.5	25	67	US-60-233-166-1188284	Sequence 1188284,
C 777	12.2	55.5	25	36	US-09-954-427-405849	Sequence 405849,	C 850	12.2	55.5	25	67	US-60-233-166-1188284	Sequence 1188284,
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C 779	12.2	55.5	25	36	US-09-954-427-405849	Sequence 405849,	C 852	12.2	55.5	25	67	US-60-233-166-195631	Sequence 195631,
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C 783	12.2	55.5	25	36	US-09-956-584-6580	Sequence 6580, Ap	C 856	12.2	55.5	25	67	US-60-233-166-210470	Sequence 210470,
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C 785	12.2	55.5	25	36	US-09-956-584-86713	Sequence 86713, A	C 858	12.2	55.5	25	67	US-60-233-166-236403	Sequence 236403,
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C 792	12.2	55.5	25	36	US-09-956-584-277779	Sequence 277779,	865	12.2	55.5	25	67	US-60-233-166-284272	Sequence 284272,
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C 799	12.2	55.5	25	36	US-09-956-584-451642	Sequence 451642,	C 872	12.2	55.5	25	67	US-60-233-166-297318	Sequence 297318,
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C 804	12.2	55.5	25	36	US-09-956-584-482251	Sequence 482251,	877	12.2	55.5	25	67	US-60-233-166-391130	Sequence 391130,
C 805	12.2	55.5	25	36	US-09-956-584-482252	Sequence 482252,	C 878	12.2	55.5	25	67	US-60-233-166-391130	Sequence 391130,
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C 814	12.2	55.5	25	36	US-09-956-584-483302	Sequence 483302,	887	12.2	55.5	25	67	US-60-234-011-119819	Sequence 119819,
C 815	12.2	55.5	25	36	US-09-956-584-531565	Sequence 531565,	C 888	12.2	55.5	25	67	US-60-234-011-119819	Sequence 119819,
C 816	12.2	55.5	25	36	US-09-956-584-531565	Sequence 531565,	889	12.2	55.5	25	67	US-60-234-011-219111	Sequence 219111,
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C 819	12.2	55.5	25	36	US-09-956-584-531570	Sequence 531570,	C 892	12.2	55.5	25	67	US-60-234-011-219508	Sequence 219508,
C 820	12.2	55.5	25	36	US-09-956-584-593778	Sequence 593778,	893	12.2	55.5	25	67	US-60-234-011-221831	Sequence 221831,
C 821	12.2	55.5	25	36	US-09-956-584-593778	Sequence 593778,	C 894	12.2	55.5	25	67	US-60-234-011-221831	Sequence 221831,
C 822	12.2	55.5	25	36	US-09-956-604-15919	Sequence 15919, A	895	12.2	55.5	25	67	US-60-234-011-270124	Sequence 270124,
C 823	12.2	55.5	25	36	US-09-956-604-15919	Sequence 15919, A	C 896	12.2	55.5	25	67	US-60-234-011-270124	Sequence 270124,
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C 900	12.2	55.5	25	67	US-60-234-017-304224	Sequence 304224,
C 901	12.2	55.5	25	67	US-60-234-017-396510	Sequence 396510,
C 902	12.2	55.5	25	67	US-60-234-017-396510	Sequence 396510,
C 903	12.2	55.5	25	67	US-60-234-017-396514	Sequence 396514,
C 904	12.2	55.5	25	67	US-60-234-017-396514	Sequence 396514,
C 905	12.2	55.5	25	67	US-60-234-017-435576	Sequence 435576,
C 906	12.2	55.5	25	67	US-60-234-017-435576	Sequence 435576,
C 907	12.2	55.5	25	67	US-60-234-017-466173	Sequence 466173,
C 908	12.2	55.5	25	67	US-60-234-017-466173	Sequence 466173,
C 909	12.2	55.5	25	67	US-60-234-017-466174	Sequence 466174,
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C 914	12.2	55.5	25	67	US-60-234-017-467610	Sequence 467610,
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C 916	12.2	55.5	25	67	US-60-234-017-467615	Sequence 467615,
C 917	12.2	55.5	25	67	US-60-234-017-467617	Sequence 467617,
C 918	12.2	55.5	25	67	US-60-234-017-467617	Sequence 467617,
C 919	12.2	55.5	25	67	US-60-234-017-526777	Sequence 526777,
C 920	12.2	55.5	25	67	US-60-234-017-526777	Sequence 526777,
C 921	12.2	55.5	25	67	US-60-234-017-526781	Sequence 526781,
C 922	12.2	55.5	25	67	US-60-234-017-526781	Sequence 526781,
C 923	12.2	55.5	25	67	US-60-234-017-604100	Sequence 604100,
C 924	12.2	55.5	25	67	US-60-234-017-604100	Sequence 604100,
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C 950	12.2	55.5	25	79	US-60-353-987-320106	Sequence 320106, A
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C 954	12.2	55.5	25	79	US-60-353-987-380477	Sequence 380477, A
C 955	12.2	55.5	25	79	US-60-353-987-440395	Sequence 440395, A
C 956	12.2	55.5	25	79	US-60-353-987-440395	Sequence 440395, A
C 957	12.2	55.5	25	79	US-60-353-987-441205	Sequence 441205, A
C 958	12.2	55.5	25	79	US-60-353-987-441205	Sequence 441205, A
C 959	12.2	55.5	25	79	US-60-353-987-489557	Sequence 489557, A
C 960	12.2	55.5	25	79	US-60-353-987-489557	Sequence 489557, A
C 961	12.2	55.5	25	79	US-60-353-987-496758	Sequence 496758, A
C 962	12.2	55.5	25	79	US-60-353-987-496758	Sequence 496758, A
C 963	12.2	55.5	25	79	US-60-353-987-502651	Sequence 502651, A
C 964	12.2	55.5	25	79	US-60-353-987-502651	Sequence 502651, A
C 965	12.2	55.5	25	79	US-60-353-987-518246	Sequence 518246, A
C 966	12.2	55.5	25	79	US-60-353-987-518246	Sequence 518246, A
C 967	12.2	55.5	25	79	US-60-353-987-519250	Sequence 519250, A
C 968	12.2	55.5	25	79	US-60-353-987-519250	Sequence 519250, A
C 969	12.2	55.5	25	79	US-60-353-987-537946	Sequence 537946, A
C 970	12.2	55.5	25	79	US-60-353-987-537946	Sequence 537946, A

771 12.2 55.5 25 79 US-60-353-987-542746 Sequence 542746,

C 972 12.2 55.5 25 79 US-60-353-987-542746 Sequence 542746,

C 973 12.2 55.5 25 79 US-60-353-987-543144 Sequence 543144,

C 974 12.2 55.5 25 79 US-60-353-987-543144 Sequence 543144,

C 975 12.2 55.5 25 79 US-60-353-987-549239 Sequence 549239,

C 976 12.2 55.5 25 79 US-60-353-987-549239 Sequence 549239,

C 977 12.2 55.5 25 79 US-60-353-987-551339 Sequence 551339,

C 978 12.2 55.5 25 79 US-60-353-987-551339 Sequence 551339,

C 979 12.2 55.5 25 79 US-60-353-987-559691 Sequence 559691,

C 980 12.2 55.5 25 79 US-60-353-987-559691 Sequence 559691,

C 981 12.2 55.5 25 79 US-60-353-987-563432 Sequence 563432,

C 982 12.2 55.5 25 79 US-60-353-987-563432 Sequence 563432,

C 983 12.2 55.5 25 79 US-60-353-987-575732 Sequence 575732,

C 984 12.2 55.5 25 79 US-60-353-987-575732 Sequence 575732,

C 985 12.2 55.5 25 79 US-60-353-987-600912 Sequence 600912,

C 986 12.2 55.5 25 79 US-60-353-987-600912 Sequence 600912,

C 987 12.2 55.5 25 79 US-60-353-987-628961 Sequence 628961,

C 988 12.2 55.5 25 79 US-60-353-987-628961 Sequence 628961,

C 989 12.2 55.5 25 79 US-60-353-987-637134 Sequence 637134,

C 990 12.2 55.5 25 79 US-60-353-987-637134 Sequence 637134,

C 991 12.2 55.5 25 79 US-60-353-987-637801 Sequence 637801,

C 992 12.2 55.5 25 79 US-60-353-987-637801 Sequence 637801,

C 993 12.2 55.5 25 79 US-60-353-987-678049 Sequence 678049,

C 994 12.2 55.5 25 79 US-60-353-987-678049 Sequence 678049,

C 995 12.2 55.5 25 79 US-60-353-987-678050 Sequence 678050,

C 996 12.2 55.5 25 79 US-60-353-987-678050 Sequence 678050,

C 997 12.2 55.5 25 79 US-60-353-987-784176 Sequence 784176,

C 998 12.2 55.5 25 79 US-60-353-987-784176 Sequence 784176,

C 999 12.2 55.5 25 79 US-60-353-987-849294 Sequence 849294,

C1000 12.2 55.5 25 79 US-60-353-987-849294 Sequence 849294,

ALIGNMENTS

RESULT 1

Sequence 1, Application US/09056363

GENERAL INFORMATION:

APPLICANT: Goodwin et al.

TITLE OF INVENTION: Production of Functional Proteins:

TITLE OF INVENTION: Balance of Shear Stress and Gravity

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: James M. Cate, NASA Johnson Space Center

STREET: 2101 NASA Road 1, Mail Code: HA

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77058-3696

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb floppy disk

COMPUTER: PC

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,363

FILING DATE: April 7, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/043,205

FILING DATE: April 8, 1997

ATTORNEY/AGENT INFORMATION:

NAME: James M. Cate

REGISTRATION NUMBER: 25,181

REFERENCE/DOCKET NUMBER: MSC-22859-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (281)483-1001

TELEFAX: (281)244-8452

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 bp

TYPE: nucleic acid

STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-09-056-363-1

Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCAG 22
DB 1 CTGAGACCGATATCGGTCTCAG 22

RESULT 2
US-09-056-363-1/c
Sequence 1, Application US/09056363
GENERAL INFORMATION:
APPLICANT: Goodwin et al.
TITLE OF INVENTION: Production of Functional Proteins:
TITLE OF INVENTION: Balance of Shear Stress and Gravity
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Cate, NASA Johnson Space Center
STREET: 2101 NASA Road 1, Mail code: HA
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77058-3696
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,363
FILING DATE: April 7, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/043,205
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: James M. Cate
REGISTRATION NUMBER: 25,181
REFERENCE/DOCKET NUMBER: MSC-22859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (281)483-1001
TELEFAX: (281)244-8452
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 bp
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:

US-09-056-363-1

Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCAG 22
DB 22 CTGAGACCGATATCGGTCTCAG 1

RESULT 3
US-09-532-001-1
Sequence 1, Application US/09532001
GENERAL INFORMATION:
APPLICANT: Goodwin et al.
TITLE OF INVENTION: Production of Functional Proteins:
TITLE OF INVENTION: Balance of Shear Stress and Gravity
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Cate, NASA Johnson Space Center
STREET: 2101 NASA Road 1, Mail code: HA
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77058-3696
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,001
FILING DATE: 21-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056,363
FILING DATE: April 7, 1998
APPLICATION NUMBER: 60/043,205
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: James M. Cate
REGISTRATION NUMBER: 25,181
REFERENCE/DOCKET NUMBER: MSC-22859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (281)483-1001
TELEFAX: (281)244-8452
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 bp
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-532-001-1
Query Match 100.0%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCAG 22
DB 1 CTGAGACCGATATCGGTCTCAG 22

RESULT 4
US-09-532-001-1/c
Sequence 1, Application US/09532001
GENERAL INFORMATION:
APPLICANT: Goodwin et al.
TITLE OF INVENTION: Production of Functional Proteins:
Balance of Shear Stresses and Gravity
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Cate, NASA Johnson Space Center
STREET: 2101 NASA Road 1, Mail code: HA
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77058-3696
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532.001
FILING DATE: 21-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056.363
FILING DATE: April 7, 1998
APPLICATION NUMBER: 60/043.205
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: James M. Cate
REGISTRATION NUMBER: 25,181
REFERENCE/DOCKET NUMBER: MSC-22859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (281) 483-1001
TELEFAX: (281) 244-8452
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 22 bp
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-532-001-1

Query Match 100.0%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGCTCTCAG 22
Db 22 CTGAGACCGATATCGCTCTCAG 1

RESULT 5
US-09-956-584-245934
Sequence 245934, Application US/09956584
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
FILE REFERENCE: 3115.1

CURRENT APPLICATION NUMBER: US/09/956.584
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234.017
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 245934
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-956-584-245934

Query Match 71.8%; Score 15.8; DB 36; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 AGACCGATATCGCTCTCAG 22
Db 6 AGACCGGATATCGCTCTCAG 24

RESULT 6
US-09-956-584-245934/c
Sequence 245934, Application US/09956584
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
FILE REFERENCE: 3115.1
CURRENT APPLICATION NUMBER: US/09/956.584
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234.017
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 245934
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-956-584-245934

Query Match 71.8%; Score 15.8; DB 36; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGCTCT 19
Db 24 CAGAGACCGATATCGCTCT 6

RESULT 7
US-60-234-017-201611
Sequence 201611, Application US/60234017
GENERAL INFORMATION:
APPLICANT: Miltman, M
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234.017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 201611
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AA823028
US-60-234-017-201611

Query Match 71.8%; Score 15.8; DB 67; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```
RESULT 13
US-09-954-429A-18545
; Sequence 18545, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-18545

Query Match      66.4%; Score 14.6; DB 36; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAGACCGGATATCGGTCTCAG 22
DB      5 TGAGACTGACCCCGGTCTCAG 25

RESULT 14
US-09-954-429A-18545/c
; Sequence 18545, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-18545

Query Match      66.4%; Score 14.6; DB 36; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGAGACCGGATATCGGTCTCA 21
DB      25 CTGAGACCGGGGTCTCAGTCTCA 5

RESULT 15
US-60-233-166-371667
; Sequence 371667, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371667
; LENGTH: 25
```

```
TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-166-371667

Query Match      66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAGACCGGATATCGGTCTCAG 22
DB      5 TGAGACTGACCCCGGTCTCAG 25

RESULT 16
US-60-233-166-371667/c
; Sequence 371667, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371667
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-166-371667

Query Match      66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGAGACCGGATATCGGTCTCA 21
DB      25 CTGAGACCGGGGTCTCAGTCTCA 5

RESULT 17
US-60-233-357-20470
; Sequence 20470, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-357-20470

Query Match      66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAGACCGGATATCGGTCTCAG 22
DB      5 TGAGACTGACCCCGGTCTCAG 25
```

```
RESULT 18
US-60-233-357-20470/c
; Sequence 20470, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methode of Genetic Analysis of Rat
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-357-20470

Query Match
Best Local Similarity 66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGGATATCGCTCTCA 21
DB 25 CTGAGACCGGCGGTCTCTCA 5

RESULT 19
US-60-233-620-99732
; Sequence 99732, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methode of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99732
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF069497
US-60-233-620-99732

Query Match
Best Local Similarity 66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGGATATCGCTCTCA 21
DB 4 CCGATACAGATATAGGTCTCA 24

RESULT 20
US-60-233-620-99732/c
; Sequence 99732, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methode of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
```

```
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99732
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF069497
US-60-233-620-99732

Query Match
Best Local Similarity 66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGAGACCGGATATCGCTCTCA 22
DB 24 TGAGACCGGATATCGCTCTCA 4

RESULT 21
US-09-956-584-216321
; Sequence 216321, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 216321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-216321

Query Match
Best Local Similarity 65.5%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GACCGATATCGCTCTC 20
DB 5 GACCGAATCGCTCTC 20

RESULT 22
US-09-956-584-216321/c
; Sequence 216321, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 216321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-216321

Query Match
Best Local Similarity 65.5%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGACCGGATATCGCTC 18
DB 20 GAGACCGGATTTGGTC 5
```

RESULT 23
US-60-234-017-216691
; Sequence 216691, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234, 017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AT789011
US-60-234-017-216691
Query Match 65.5%; Score 14.4; DB 67; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GACCGATATCGGTCTC 20
DB 5 GACCGAATCGGTCTC 20

RESULT 24
US-60-234-017-216691/c
; Sequence 216691, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234, 017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AT789011
US-60-234-017-216691
Query Match 65.5%; Score 14.4; DB 67; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GAGACCGATATCGGTCTC 18
DB 20 GAGACCGATATCGGTCTC 5

RESULT 25
US-60-353-987-90477
; Sequence 90477, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353, 987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-90477
Query Match 64.5%; Score 14.2; DB 79; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 GAGACCGATATCGGTCTCA 21
DB 6 GAGACCGATATCGGTATGA 24

RESULT 26
US-60-353-987-90477/c
; Sequence 90477, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353, 987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-90477
Query Match 64.5%; Score 14.2; DB 79; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCTC 20
DB 24 TCATACCGATATGGGTCTC 6

RESULT 27
PCT-US99-10361-32
; Sequence 32, Application PC/TUS9910361
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Modulation Of Molecular Interaction Sites On RNA And Other Biomo
; FILE REFERENCE: IBIS-0144
; CURRENT APPLICATION NUMBER: PCT/US99/10361
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 32
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic RNA molecule
PCT-US99-10361-32
Query Match 64.5%; Score 14.2; DB 1; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 GAGACCGATATCGGTCTCA 21
DB 1 GAGACCCAAVUCUGUCUCA 19

RESULT 28
PCT-US99-10361-32/c
; Sequence 32, Application PC/TUS9910361
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.

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; TITLE OF INVENTION: Modulation Of Molecular Interaction Sites On RNA And Other Biomo
; FILE REFERENCE: IBIS-014
; CURRENT APPLICATION NUMBER: PCT/US99/10361
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 32
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic RNA molecule
PCT-US99-10361-32

Query Match          64.5%; Score 14.2; DB 1; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TGAGACCGATATGCGTCTC 20
        ||||| ||||| |||||
Db      19 TGAGACAGATTGGGTCTC 1

RESULT 29
; Sequence 30, Application US/09310735
; GENERAL INFORMATION:
; APPLICANT: Becker, David J
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735-30

Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 GAGACCGATATGCGTCTCA 21
        ||||| ||||| |||||
Db      1 GAGACCCAAAUUCUGUCUCA 19

RESULT 30
; Sequence 30, Application US/09310735
; GENERAL INFORMATION:
; APPLICANT: Becker, David J
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
```

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; TITLE OF INVENTION: Other Biomolecules
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735-30

Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TGAGACCGATATGCGTCTC 20
        ||||| ||||| |||||
Db      19 TGAGACAGATTGGGTCTC 1

RESULT 31
; Sequence 30, Application US/09310735A
; GENERAL INFORMATION:
; APPLICANT: Becker, David J
; APPLICANT: Crooke, Stanley T
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735A
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735A-30

Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 GAGACCGATATGCGTCTCA 21
        ||||| ||||| |||||
Db      1 GAGACCCAAAUUCUGUCUCA 19

RESULT 32
; Sequence 30, Application US/09310735A
; GENERAL INFORMATION:
; APPLICANT: Becker, David J
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
```

```

; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735A
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 28
; SEQ ID NO 30
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735A-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGAGACCGATATCGGTCTC 20
      ||||| ||||| |||||
Db      19 TGAGACGAGATTGGGTCTC 1

RESULT 33
US-09-310-735C-30
; Sequence 30, Application US/09310735C
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Swayze, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735C
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735C-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GAGACCGATATCGGTCTCA 21
      ||||| ||||| |||||
Db      1 GAGACCCAAUUCUGUCUCA 19

RESULT 34
US-09-310-735C-30/C
; Sequence 30, Application US/09310735C
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
```

```

; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735C
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735C-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGAGACCGATATCGGTCTC 20
      ||||| ||||| |||||
Db      19 TGAGACGAGATTGGGTCTC 1

RESULT 35
US-09-310-761-30
; Sequence 30, Application US/09310761
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Swayze, Eric
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: RNA And Methods Of Modulating The Same
; FILE REFERENCE: IBIS0170
; CURRENT APPLICATION NUMBER: US/09/310,761
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-761-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GAGACCGATATCGGTCTCA 21
      ||||| ||||| |||||
Db      1 GAGACCCAAUUCUGUCUCA 19

RESULT 36
US-09-310-761-30/C
; Sequence 30, Application US/09310761
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
```



```
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Swayze, Eric
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Ornithine Decarboxylase
; FILE REFERENCE: IBIS0170
; CURRENT APPLICATION NUMBER: US/09/310,761
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ. ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-761-30
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Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      2 TGAGACCGATATCGTCTC 20
        ||||| ||||| |||||
Db      19 TGAGACAGATTGGTCTC 1
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```
RESULT 37
US-09-310-762-30
; Sequence 30, Application US/09310762
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grilley, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; TITLE OF INVENTION: Methods Of Modulating The Same
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ. ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762-30
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Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 GAGACCGATATCGTCTCA 21
        ||||| ||||| |||||
Db      1 GAGACCCAUAUCUGUCUCA 19
```

```
RESULT 38
US-09-310-762-30/C
; Sequence 30, Application US/09310762
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grilley, Richard
; APPLICANT: Crooke, Stanley T
```

```
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ. ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762-30
```

```
Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 TGAGACCGATATCGTCTC 20
        ||||| ||||| |||||
Db      19 TGAGACAGATTGGTCTC 1
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RESULT 39
US-09-310-762A-30
; Sequence 30, Application US/09310762A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grilley, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; TITLE OF INVENTION: Methods Of Modulating The Same
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ. ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762A-30
```

```
Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 GAGACCGATATCGTCTCA 21
        ||||| ||||| |||||
Db      1 GAGACCCAUAUCUGUCUCA 19
```

```
RESULT 40
US-09-310-762A-30/C
; Sequence 30, Application US/09310762A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grilley, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
```

```

; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatesan
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeil, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762A
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762A-30

```

```

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      2 TGAGACCGATATCGGCTC 20
      ||||| ||| |||||
Db      19 TGAGACAGATTGGGCTC 1

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Search completed: June 14, 2003, 23:14:47
 Job time : 2140 secs

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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 22:15:00 ; Search time 661 Seconds
(without alignments)
229.931 Million cell updates/sec

Title: US-09-532-001-1
Perfect score: 22
Sequence: 1 CTGAGACCGATATCGGTCTCAG 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7791535 seqs, 3454190175 residues

Total number of hits satisfying chosen parameters: 8630676

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

Pending Patents_NA.New.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	14.8	67.3	25	9	US-10-355-577-403951, Sequence 403951, A
3	14.6	66.4	25	7	US-09-954-445A-99732, Sequence 99732, A
4	14.6	66.4	25	7	US-09-954-445A-99732, Sequence 99732, A
5	14.6	66.4	25	11	US-60-427-836-181614, Sequence 181614, A
6	14.6	66.4	25	11	US-60-427-836-181614, Sequence 181614, A
7	14.2	64.5	25	9	US-10-355-577-90477, Sequence 90477, A
8	14.2	64.5	25	9	US-10-355-577-90477, Sequence 90477, A
9	14	63.6	25	6	US-09-660-222-15526, Sequence 15526, A
10	14	63.6	25	6	US-09-660-222-15526, Sequence 15526, A
11	14	63.6	25	6	US-09-660-222-15526, Sequence 15526, A
12	14	63.6	25	6	US-09-660-222-15526, Sequence 15526, A
13	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
14	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
15	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
16	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
17	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
18	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
19	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
20	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
21	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A
22	14	63.6	25	9	US-10-098-263B-30445, Sequence 30445, A

23	14	63.6	25	9	US-10-355-577-576645, Sequence 576645, A
24	14	63.6	25	9	US-10-355-577-576645, Sequence 576645, A
25	14	63.6	25	9	US-10-355-577-802554, Sequence 802554, A
26	14	63.6	25	9	US-10-355-577-802554, Sequence 802554, A
27	13.8	62.7	25	9	US-10-355-577-320105, Sequence 320105, A
28	13.8	62.7	25	9	US-10-355-577-320105, Sequence 320105, A
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36	13.6	61.8	25	9	US-10-098-263B-93368, Sequence 93368, A
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38	13.6	61.8	25	9	US-10-355-577-404087, Sequence 404087, A
39	13.6	61.8	25	9	US-10-355-577-700753, Sequence 700753, A
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42	13.6	61.8	25	9	US-10-355-577-829330, Sequence 829330, A
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71	13	59.1	25	5	US-09-660-0808-20408, Sequence 20408, A
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73	13	59.1	25	6	US-09-660-222-15527, Sequence 15527, A
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78	13	59.1	25	7	US-09-953-570-103667, Sequence 103667, A
79	13	59.1	25	7	US-09-954-445A-21632, Sequence 21632, A
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88	13	59.1	25	9	US-10-355-577-371036, Sequence 371036, A
89	13	59.1	25	9	US-10-355-577-371036, Sequence 371036, A
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91	13	59.1	25	9	US-10-355-577-402225, Sequence 402225, A
92	13	59.1	25	9	US-10-355-577-519794, Sequence 519794, A
93	13	59.1	25	9	US-10-355-577-519794, Sequence 519794, A
94	13	59.1	25	9	US-10-355-577-631872, Sequence 631872, A
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C 97	13	59.1	25	9	US-10-355-577-875225	Sequence 875225,	C 170	12.8	58.2	25	11	US-60-427-808-905633	Sequence 905633,
C 98	13	59.1	25	9	US-10-355-577-875225	Sequence 875225,	C 171	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 99	13	59.1	25	10	US-60-469-545-35396	Sequence 35396, A	C 172	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 100	13	59.1	25	10	US-60-469-545-35396	Sequence 35396, A	C 173	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 101	13	59.1	25	10	US-60-469-545-35886	Sequence 35886, A	C 174	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 102	13	59.1	25	10	US-60-469-545-35886	Sequence 35886, A	C 175	12.6	57.3	25	6	US-09-660-222-85019	Sequence 85019, A
C 103	13	59.1	25	10	US-60-469-545-202291	Sequence 202291,	C 176	12.6	57.3	25	6	US-09-660-222-85019	Sequence 85019, A
C 104	13	59.1	25	10	US-60-469-545-202291	Sequence 202291,	C 177	12.6	57.3	25	7	US-09-954-445A-33743	Sequence 33743, A
C 105	13	59.1	25	10	US-60-469-545-202781	Sequence 202781,	C 178	12.6	57.3	25	7	US-09-954-445A-33743	Sequence 33743, A
C 106	13	59.1	25	10	US-60-469-545-202781	Sequence 202781,	C 179	12.6	57.3	25	7	US-09-954-445A-33744	Sequence 33744, A
C 107	13	59.1	25	11	US-60-427-808-380944	Sequence 380944,	C 180	12.6	57.3	25	7	US-09-954-445A-33744	Sequence 33744, A
C 108	13	59.1	25	11	US-60-427-808-380944	Sequence 380944,	C 181	12.6	57.3	25	7	US-09-954-445A-99983	Sequence 99983, A
C 109	13	59.1	25	11	US-60-427-808-509558	Sequence 509558,	C 182	12.6	57.3	25	7	US-09-954-445A-99983	Sequence 99983, A
C 110	13	59.1	25	11	US-60-427-808-509558	Sequence 509558,	C 183	12.6	57.3	25	7	US-09-954-445A-99983	Sequence 99983, A
C 111	13	59.1	25	11	US-60-427-808-689447	Sequence 689447,	C 184	12.6	57.3	25	7	US-09-954-445A-128650	Sequence 128650,
C 112	13	59.1	25	11	US-60-427-808-689447	Sequence 689447,	C 185	12.6	57.3	25	7	US-09-954-445A-128651	Sequence 128651,
C 113	13	59.1	25	11	US-60-427-808-734492	Sequence 734492,	C 186	12.6	57.3	25	7	US-09-954-445A-128651	Sequence 128651,
C 114	13	59.1	25	11	US-60-427-808-734492	Sequence 734492,	C 187	12.6	57.3	25	7	US-10-098-263B-110373	Sequence 110373,
C 115	13	59.1	25	11	US-60-427-808-851327	Sequence 851327,	C 188	12.6	57.3	25	9	US-10-098-263B-110373	Sequence 110373,
C 116	13	59.1	25	11	US-60-427-808-851327	Sequence 851327,	C 189	12.6	57.3	25	9	US-10-355-577-5941	Sequence 5941, A
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C 120	13	59.1	25	11	US-60-427-808-181612	Sequence 181612,	C 193	12.6	57.3	25	9	US-10-355-577-90478	Sequence 90478, A
C 121	13	59.1	25	11	US-60-427-808-181612	Sequence 181612,	C 194	12.6	57.3	25	9	US-10-355-577-90478	Sequence 90478, A
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C 243	12.6	57.3	25	11	US-60-427-836-48799	Sequence 48799, A	316	12.4	56.4	25	9	US-10-355-577-579566	Sequence 579566, A
C 244	12.6	57.3	25	11	US-60-427-836-48799	Sequence 48799, A	317	12.4	56.4	25	9	US-10-355-577-608149	Sequence 608149, A
C 245	12.6	57.3	25	11	US-60-427-836-387512	Sequence 387512, A	318	12.4	56.4	25	9	US-10-355-577-608149	Sequence 608149, A
C 246	12.6	57.3	25	11	US-60-427-836-387512	Sequence 387512, A	319	12.4	56.4	25	9	US-10-355-577-626708	Sequence 626708, A
C 247	12.6	57.3	25	11	US-60-427-836-482669	Sequence 482669, A	320	12.4	56.4	25	9	US-10-355-577-626708	Sequence 626708, A
C 248	12.6	57.3	25	11	US-60-427-836-482669	Sequence 482669, A	321	12.4	56.4	25	9	US-10-355-577-802553	Sequence 802553, A
C 249	12.6	57.3	25	11	US-60-427-836-504798	Sequence 504798, A	322	12.4	56.4	25	9	US-10-355-577-802553	Sequence 802553, A
C 250	12.6	57.3	25	11	US-60-427-836-504798	Sequence 504798, A	323	12.4	56.4	25	9	US-10-355-577-814469	Sequence 814469, A
C 251	12.6	57.3	25	11	US-60-427-836-504799	Sequence 504799, A	324	12.4	56.4	25	9	US-10-355-577-814469	Sequence 814469, A
C 252	12.6	57.3	25	11	US-60-427-836-504799	Sequence 504799, A	325	12.4	56.4	25	9	US-10-355-577-814470	Sequence 814470, A
C 253	12.6	57.3	50	1	PCT-US03-13015-879	Sequence 879, App	326	12.4	56.4	25	9	US-10-355-577-814470	Sequence 814470, A
C 254	12.6	57.3	50	1	PCT-US03-13015-879	Sequence 879, App	327	12.4	56.4	25	9	US-10-355-577-825522	Sequence 825522, A
C 255	12.6	57.3	50	9	US-10-325-899-2060	Sequence 2060, Ap	328	12.4	56.4	25	9	US-10-355-577-825522	Sequence 825522, A
C 256	12.6	57.3	50	9	US-10-325-899-2060	Sequence 2060, Ap	329	12.4	56.4	25	9	US-10-355-577-923571	Sequence 923571, A
C 257	12.4	56.4	21	9	US-10-035-9788A-33	Sequence 33, Appl	330	12.4	56.4	25	9	US-10-355-577-923571	Sequence 923571, A
C 258	12.4	56.4	21	9	US-10-035-9788A-33	Sequence 33, Appl	331	12.4	56.4	25	9	US-10-355-577-954030	Sequence 954030, A
C 259	12.4	56.4	25	5	US-09-660-080B-10772	Sequence 10272, A	332	12.4	56.4	25	9	US-60-470-475-93594	Sequence 93594, A
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C 262	12.4	56.4	25	6	US-09-660-222-62449	Sequence 62449, A	335	12.4	56.4	25	10	US-60-470-475-100402	Sequence 100402, A
C 263	12.4	56.4	25	6	US-09-660-222-62455	Sequence 62455, A	336	12.4	56.4	25	10	US-60-417-190-16466	Sequence 16466, A
C 264	12.4	56.4	25	6	US-09-660-222-62455	Sequence 62455, A	337	12.4	56.4	25	11	US-60-417-190-16466	Sequence 16466, A
C 265	12.4	56.4	25	6	US-09-660-222-114462	Sequence 114462, A	338	12.4	56.4	25	11	US-60-417-190-16466	Sequence 16466, A
C 266	12.4	56.4	25	6	US-09-660-222-114462	Sequence 114462, A	339	12.4	56.4	25	11	US-60-417-190-16466	Sequence 16466, A
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C 270	12.4	56.4	25	6	US-09-660-222-139083	Sequence 139083, A	343	12.4	56.4	25	11	US-60-427-808-313509	Sequence 313509, A
C 271	12.4	56.4	25	7	US-09-953-570-137844	Sequence 137844, A	344	12.4	56.4	25	11	US-60-427-808-313509	Sequence 313509, A
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C 275	12.4	56.4	25	9	US-10-098-263B-21859	Sequence 21859, A	348	12.4	56.4	25	11	US-60-427-808-389384	Sequence 389384, A
C 276	12.4	56.4	25	9	US-10-098-263B-21859	Sequence 21859, A	349	12.4	56.4	25	11	US-60-427-808-734095	Sequence 734095, A
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C 280	12.4	56.4	25	9	US-10-098-263B-70456	Sequence 70456, A	353	12.4	56.4	25	11	US-60-427-808-832054	Sequence 832054, A
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C 282	12.4	56.4	25	9	US-10-098-263B-87626	Sequence 87626, A	355	12.4	56.4	25	11	US-60-427-808-832292	Sequence 832292, A
C 283	12.4	56.4	25	9	US-10-098-263B-99206	Sequence 99206, A	356	12.4	56.4	25	11	US-60-427-808-832292	Sequence 832292, A
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C 291	12.4	56.4	25	9	US-10-355-577-194918	Sequence 194918, A	364	12.4	56.4	25	11	US-60-427-835-218811	Sequence 218811, A
C 292	12.4	56.4	25	9	US-10-355-577-194918	Sequence 194918, A	365	12.4	56.4	25	11	US-60-427-835-218811	Sequence 218811, A
C 293	12.4	56.4	25	9	US-10-355-577-16826	Sequence 316226, A	366	12.4	56.4	25	11	US-60-427-835-595782	Sequence 595782, A
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C 295	12.4	56.4	25	9	US-10-355-577-339261	Sequence 339261, A	368	12.4	56.4	45	6	US-09-939-471-13	Sequence 13, Appl
C 296	12.4	56.4	25	9	US-10-355-577-387487	Sequence 387487, A	369	12.2	55.5	20	9	US-10-310-188-36880	Sequence 36880, A
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C 300	12.4	56.4	25	9	US-10-355-577-399725	Sequence 399725, A	373	12.2	55.5	25	6	US-09-660-222-81573	Sequence 81573, A
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C 304	12.4	56.4	25	9	US-10-355-577-474743	Sequence 474743, A	377	12.2	55.5	25	7	US-09-660-222-81573	Sequence 81573, A
C 305	12.4	56.4	25	9	US-10-355-577-474743	Sequence 474743, A	378	12.2	55.5	25	7	US-09-660-222-81573	Sequence 81573, A
C 306	12.4	56.4	25	9	US-10-355-577-475721	Sequence 475721, A	379	12.2	55.5	25	7	US-09-660-222-81573	Sequence 81573, A
C 307	12.4	56.4	25	9	US-10-355-577-475721	Sequence 475721, A	380	12.2	55.5	25	7	US-09-660-222-81573	Sequence 81573, A
C 308	12.4	56.4	25	9	US-10-355-577-475722	Sequence 475722, A	381	12.2	55.5	25	9	US-10-098-263B-77815	Sequence 77815, A
C 309	12.4	56.4	25	9	US-10-355-577-482340	Sequence 482340, A	382	12.2	55.5	25	9	US-10-098-263B-77815	Sequence 77815, A
C 310	12.4	56.4	25	9	US-10-355-577-482340	Sequence 482340, A	383	12.2	55.5	25	9	US-10-098-263B-77815	Sequence 77815, A
C 311	12.4	56.4	25	9	US-10-355-577-576637	Sequence 576637, A	384	12.2	55.5	25	9	US-10-098-263B-77815	Sequence 77815, A
C 312	12.4	56.4	25	9	US-10-355-577-576637	Sequence 576637, A	385	12.2	55.5	25	9	US-10-098-263B-77815	Sequence 77815, A
C 313	12.4	56.4	25	9	US-10-355-577-576646	Sequence 576646, A	386	12.2	55.5	25	9	US-10-098-263B-103542	Sequence 103542, A
C 314	12.4	56.4	25	9	US-10-355-577-576646	Sequence 576646, A	387	12.2	55.5	25	9	US-10-098-263B-103542	Sequence 103542, A

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C 828	11.8	53.6	25	9	US-10-355-577-788843	Sequence 788843,	C 901	11.6	52.7	25	6	US-09-660-222-76228	Sequence 76228, A
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ALIGNMENTS

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RESULT 1
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; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
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Best Local Similarity 88.9%; Pred. No. 1.4e+03;
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; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-403951
Query Match 67.3%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 GAGACCGATATCGGTCTC 20
Db 2 GAGACCGATATCGGTCTC 19

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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-403951
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Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 19 GAGACCGATATCGGTCTC 2

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; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 99732
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-99732
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Best Local Similarity 81.0%; Pred. No. 1.8e+03;
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RESULT 4
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; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 99732
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US-09-954-445A-99732
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Best Local Similarity 81.0%; Pred. No. 1.8e+03;
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; GENERAL INFORMATION:

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 181614
; LENGTH: 25
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; ORGANISM: Rattus norvegicus
US-60-427-836-181614
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Db      5 CTGAGACCGATATCGAGGCA 25
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```
RESULT 6
US-60-427-836-181614/c
; Sequence 181614, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 181614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-181614
```

```
Query Match      66.4%; Score 14.6; DB 11; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 TGAGACCGATATCGGTCTCAG 22
      |||||
Db      25 TGCTCCATATCGGTCTCAG 5
```

```
RESULT 7
US-10-355-577-90477
; Sequence 90477, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-90477
```

```
Query Match      64.5%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 GAGACCGATATCGGTCTCA 21
      |||||
Db      6 GAGACCGATATCGGTATGA 24
```

```
RESULT 8
US-10-355-577-90477/c
; Sequence 90477, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-90477
```

```
Query Match      64.5%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 TGAGACCGATATCGGTCTC 20
      |||||
Db      24 TCATACCGATATCGGTCTC 6
```

```
RESULT 9
US-09-660-222-15526
; Sequence 15526, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D87073
US-09-660-222-15526
```

```
Query Match      63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 GATATCGGTCTCAG 22
      |||||
Db      1 GATATCGGTCTCAG 14
```

```
RESULT 10
US-09-660-222-15526/c
; Sequence 15526, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15526
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D87073
US-09-660-222-15526

Query Match          63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATC 14
Db 14 CTGAGACCGATATC 1

RESULT 11
US-09-660-222-74211
; Sequence 74211, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00951
US-09-660-222-74211

Query Match          63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
Db 2 CTGATACCAATATGATGCTCCG 23

RESULT 12
US-09-660-222-74211/c
; Sequence 74211, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00951
US-09-660-222-74211

Query Match          63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
Db 2 CTGATACCAATATGATGCTCCG 23
```

```
Qy 1 CTGAGACCGATATCGTCTCAG 22
Db 23 CGGAGACTCATATGCTATCAG 2

RESULT 13
US-10-098-263B-30445
; Sequence 30445, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
Db 3 CTCTACCGATATGCTCTCAG 24

RESULT 14
US-10-098-263B-30445/c
; Sequence 30445, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
Db 24 CTGAGACAATATCGTAGAG 3

RESULT 15
US-10-098-263B-70455
; Sequence 70455, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 GATATCGGTCTCAG 22
    |||||
Db 5 GATATCGGTCTCAG 18
```

```
RESULT 16
US-10-098-263B-70455/c
; Sequence 70455, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATC 14
    |||||
Db 18 CTGAGACCGATATC 5
```

```
RESULT 17
US-10-098-263B-87625
; Sequence 87625, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATCGTCTCAG 22
    |||||
Db 2 CTGATACCATATGAGTCTCCG 23
```

RESULT 18

```
US-10-098-263B-87625/c
; Sequence 87625, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATCGTCTCAG 22
    |||||
Db 23 CGGAGACTCATATGCGTATCAG 2
```

```
RESULT 19
US-10-098-263B-105385
; Sequence 105385, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 GATATCGGTCTCAG 22
    |||||
Db 1 GATATCGGTCTCAG 14
```

```
RESULT 20
US-10-098-263B-105385/c
; Sequence 105385, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385
```

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATC 14
|||||
Db 14 CTGAGACCGATATC 1

RESULT 21
US-10-355-577-316225
; Sequence 316225, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 316225
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-316225

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATATCGTCTCAG 22
|||||
Db 4 GATATCGTCTCAG 17

RESULT 22
US-10-355-577-316225/C
; Sequence 316225, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 316225
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-316225

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATC 14
|||||
Db 17 CTGAGACCGATATC 4

RESULT 23
US-10-355-577-576645
; Sequence 576645, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 576645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-576645

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATATCGTCTCAG 22
|||||
Db 1 GATATCGTCTCAG 14

RESULT 24
US-10-355-577-576645/C
; Sequence 576645, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 576645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-576645

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATC 14
|||||
Db 14 CTGAGACCGATATC 1

RESULT 25
US-10-355-577-802554
; Sequence 802554, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 802554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-802554

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATATCGTCTCAG 22
|||||
Db 5 GATATCGTCTCAG 18

RESULT 26
US-10-355-577-802554/C
; Sequence 802554, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

```
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 802554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-802554
```

```
Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATC 14
Db 18 CTGAGACCGATATC 5
```

RESULT 27

```
US-10-355-577-320105
; Sequence 320105, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-320105
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 GACCGATATCGGTCTCA 21
Db 8 GACCGATATCGGTCTCA 24
```

```
RESULT 28
US-10-355-577-320105/c
; Sequence 320105, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-320105
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 TGAGACCGATATCGGTCTC 18
Db 24 TGAGATCGATATCTCTCTC 8
```

RESULT 29

```
US-10-355-577-559692
; Sequence 559692, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 559692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-559692
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 GAGACCGATATCGGTCTC 19
Db 1 GAGACCGATATCGGTCTC 17
```

```
RESULT 30
US-10-355-577-559692/c
; Sequence 559692, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 559692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-559692
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 AGACCGATATCGGTCTC 20
Db 17 AGACCGATATCGGTCTC 1
```

```
RESULT 31
US-09-954-445A-48359
; Sequence 48359, Application US/0995445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48359
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-48359
```

```
Query Match 61.8%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

OY 2 TGAGACCGATATCGGTCTCA 21
Db 2 TCAGACGATATTCGCTCGCA 21

RESULT 32
US-09-954-445A-48359/C
; Sequence 48359, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48359
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-48359

Query Match 61.8%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCTCA 21
Db 21 TCGACCGATATTCGCTCTGA 2

RESULT 33
US-10-098-263B-67902
; Sequence 67902, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCTC 20
Db 4 CGGAGACGAGATTTCGCTCGC 23

RESULT 34
US-10-098-263B-67902/C
; Sequence 67902, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GAGACCGATATCGGTCTCAG 22
Db 23 GCGACCGAATTCGTCTCCG 4

RESULT 35
US-10-098-263B-93368
; Sequence 93368, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCTC 20
Db 2 CGGAGACGAGTTATCGGTCTG 21

RESULT 36
US-10-098-263B-93368/C
; Sequence 93368, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GAGACCGATATCGGTCTCAG 22
Db 21 GCGACCGAATTCGTCTCCG 2


```
RESULT 37
US-10-355-577-404087
; Sequence 404087, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 404087
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-404087

Query Match          61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGTCTCAG 22
Db 2 GAGACCGATATCGGACTCGG 21

RESULT 38
US-10-355-577-404087/C
; Sequence 404087, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 404087
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-404087

Query Match          61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTC 20
Db 21 CCGAGTCGGGTATCCGTCTC 2

RESULT 39
US-10-355-577-700753
; Sequence 700753, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 700753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-700753

Query Match          61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTC 20
Db 21 CCGAGTCGGGTATCCGTCTC 2

Query Match          61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 3 GAGACCGATATCGTCTCAG 22
Db 4 GATACCGCTATAGTCTCAG 23

RESULT 40
US-10-355-577-700753/C
; Sequence 700753, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 700753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-700753

Query Match          61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTC 20
Db 23 CTGAGACCTATTAAGGTATC 4
```

Search completed: June 14, 2003, 23:26:57
Job time : 667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 09:51:10 ; Search time 979 Seconds
(without alignments)
653.996 Million cell updates/sec

Title: US-09-532-001-1

Perfect score: 22

Sequence: 1 CTGAGACCGATATCGGTCTCAG 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rtd:*

36: em_hcg_man:*

37: em_hcg_vrl:*

38: em_sy:*

39: em_hlgo_hum:*

40: em_hlgo_mus:*

41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.4	60.9	20	6	AX295560 Sequence
2	13.4	60.9	20	6	AX295560 Sequence
3	13.4	60.9	24	6	AX290927 Sequence
4	13.4	60.9	24	6	AX290927 Sequence
5	13	59.1	44	6	AR161400 Sequence
6	13	59.1	44	6	AR161400 Sequence
7	12.6	57.3	24	6	AX292255 Sequence
8	12.6	57.3	24	6	AX292255 Sequence
9	12.6	57.3	25	6	AX189358 Sequence
10	12.6	57.3	25	6	AX189358 Sequence
11	12.4	56.4	21	6	BD009441 Probes, m
12	12.4	56.4	21	6	BD009441 Probes, m
13	12.4	56.4	30	6	BD009441 Probes, m
14	12.4	56.4	30	6	BD009441 Probes, m
15	12.4	56.4	32	6	AX1659 Sequence 26
16	12.4	56.4	32	6	AX1659 Sequence 26
17	12.4	56.4	45	6	AX361282 Sequence
18	12.4	56.4	45	6	AX361282 Sequence
19	12.2	55.5	24	6	AX047302 Sequence
20	12.2	55.5	24	6	AX047302 Sequence
21	12.2	55.5	26	6	AX047302 Sequence
22	12.2	55.5	26	6	E06104 Oligonucleo
23	12.2	55.5	26	6	E06104 Oligonucleo
24	12.2	55.5	26	6	E10842 PCR primer
25	12.2	55.5	26	6	E10842 PCR primer
26	12.2	55.5	33	6	AR120578 Sequence
27	12.2	55.5	33	6	AR120578 Sequence
28	12.2	55.5	33	6	AR120579 Sequence
29	12.2	55.5	33	6	AR120579 Sequence
30	12.2	55.5	33	6	IR3498 Sequence 1
31	12.2	55.5	33	6	IR3498 Sequence 1
32	12.2	55.5	37	6	AX099887 Sequence
33	12.2	55.5	37	6	AX099887 Sequence
34	12.2	55.5	37	6	AX138008 Sequence
35	12.2	55.5	39	6	AR120598 Sequence
36	12.2	55.5	39	6	AR120598 Sequence
37	12.2	55.5	39	6	AR120599 Sequence
38	12.2	55.5	39	6	AR120599 Sequence
39	12.2	55.5	28	6	AR120599 Sequence
40	12	54.5	28	6	IR27047 Sequence 68
41	12	54.5	28	6	IR27047 Sequence 68
42	12	54.5	28	6	IR27048 Sequence 69
43	12	54.5	28	6	IR27048 Sequence 69
44	12	54.5	37	6	IR3695 Sequence 3
45	11.8	53.6	21	6	AX096000 Sequence
46	11.8	53.6	21	6	AX096000 Sequence
47	11.8	53.6	34	6	AR120591 Sequence
48	11.8	53.6	34	6	AR120591 Sequence
49	11.8	53.6	45	6	AR13920 Nucleotide
50	11.8	53.6	45	6	AR13920 Nucleotide
51	11.8	53.6	45	6	AR005067 Sequence
52	11.8	53.6	45	6	AR005067 Sequence
53	11.8	53.6	45	6	AR060883 Sequence
54	11.8	53.6	45	6	AR060883 Sequence
55	11.8	53.6	45	6	AR10817 Sequence
56	11.8	53.6	45	6	AR10817 Sequence
57	11.8	53.6	45	6	IR18296 Sequence 43
58	11.8	53.6	45	6	IR18296 Sequence 43
59	11.8	53.6	45	6	IR24509 Sequence 41
60	11.8	53.6	45	6	IR24509 Sequence 41
61	11.8	53.6	45	6	IR28903 Sequence 41
62	11.8	53.6	45	6	IR28903 Sequence 41
63	11.8	53.6	45	6	IR3041 Sequence 41
64	11.8	53.6	45	6	IR3041 Sequence 41
65	11.8	53.6	45	6	IR9637 Sequence 41

C 66	11.8	53.6	45	6	179637	179637 Sequence 41	139	11.2	50.9	24	6	AR035478	AR035478 Sequence
C 67	11.6	52.7	21	6	BD009419	BD009419 Probes, m	C 140	11.2	50.9	24	6	AR035478	AR035478 Sequence
C 68	11.6	52.7	21	6	BD009419	BD009419 Probes, m	C 141	11.2	50.9	26	6	AX038074	AX038074 Sequence
C 69	11.6	52.7	38	6	AX218602	AX218602 Sequence	C 142	11.2	50.9	26	6	AX038074	AX038074 Sequence
C 70	11.6	52.7	38	6	AX218602	AX218602 Sequence	C 143	11.2	50.9	26	6	AX038075	AX038075 Sequence
C 71	11.6	52.7	48	6	117682	117682 Sequence 10	C 144	11.2	50.9	26	6	AX038075	AX038075 Sequence
C 72	11.6	52.7	48	6	117682	117682 Sequence 10	C 145	11.2	50.9	29	6	AR160337	AR160337 Sequence
C 73	11.4	51.8	18	6	AR058964	AR058964 Sequence	C 146	11.2	50.9	29	6	AR160337	AR160337 Sequence
C 74	11.4	51.8	18	6	AR058964	AR058964 Sequence	C 147	11.2	50.9	33	6	AX060822	AX060822 Sequence
C 75	11.4	51.8	18	6	AR058964	AR058964 Sequence	C 148	11.2	50.9	33	6	AX060822	AX060822 Sequence
C 76	11.4	51.8	18	6	AR105238	AR105238 Sequence	C 149	11.2	50.9	40	9	HS274607	HS274607 Sequence
C 77	11.4	51.8	18	6	AR119159	AR119159 Sequence	C 150	11.2	50.9	40	9	HS274607	HS274607 Sequence
C 78	11.4	51.8	18	6	AR119159	AR119159 Sequence	C 151	11.2	50.9	20	6	E06077	E06077 Sequence
C 79	11.4	51.8	18	6	AR123530	AR123530 Sequence	C 152	11.2	50.0	20	6	E06077	E06077 Sequence
C 80	11.4	51.8	18	6	AR123530	AR123530 Sequence	C 153	11.2	50.0	20	6	E08908	E08908 Sequence
C 81	11.4	51.8	18	6	AR123534	AR123534 Sequence	C 154	11.2	50.0	20	6	E08908	E08908 Sequence
C 82	11.4	51.8	18	6	AR123534	AR123534 Sequence	C 155	11.2	50.0	25	6	AX447652	AX447652 Sequence
C 83	11.4	51.8	18	6	AR138183	AR138183 Sequence	C 156	11.2	50.0	25	6	AX447652	AX447652 Sequence
C 84	11.4	51.8	18	6	AR138183	AR138183 Sequence	C 157	11.2	50.0	25	6	E41780	E41780 Sequence
C 85	11.4	51.8	18	6	AR176744	AR176744 Sequence	C 158	11.2	50.0	25	6	E41780	E41780 Sequence
C 86	11.4	51.8	18	6	AR176744	AR176744 Sequence	C 159	11.2	50.0	26	6	AX110707	AX110707 Sequence
C 87	11.4	51.8	18	6	AR198315	AR198315 Sequence	C 160	11.2	50.0	26	6	AX110707	AX110707 Sequence
C 88	11.4	51.8	18	6	AR198315	AR198315 Sequence	C 161	11.2	50.0	30	6	AX128544	AX128544 Sequence
C 89	11.4	51.8	18	6	AX470016	AX470016 Sequence	C 162	11.2	50.0	30	6	AX128544	AX128544 Sequence
C 90	11.4	51.8	18	6	AX470016	AX470016 Sequence	C 163	11.2	50.0	32	6	AR003442	AR003442 Sequence
C 91	11.4	51.8	27	6	BD012174	BD012174 Antineopl	C 164	11.2	50.0	32	6	AR003442	AR003442 Sequence
C 92	11.4	51.8	27	6	BD012174	BD012174 Antineopl	C 165	11.2	50.0	36	6	I31694	I31694 Sequence 2
C 93	11.4	51.8	27	23	BD004854	BD004854 Antineopl	C 166	11.2	50.0	36	6	I31694	I31694 Sequence 2
C 94	11.4	51.8	27	23	BD004854	BD004854 Antineopl	C 167	11.2	50.0	37	6	AR183323	AR183323 Sequence
C 95	11.4	51.8	29	6	AX192024	AX192024 Sequence	C 168	11.2	50.0	37	6	AR183323	AR183323 Sequence
C 96	11.4	51.8	29	6	AX192024	AX192024 Sequence	C 169	11.2	50.0	37	6	AX049947	AX049947 Sequence
C 97	11.4	51.8	38	6	BD011790	BD011790 RNP deriv	C 170	11.2	50.0	37	6	AX049947	AX049947 Sequence
C 98	11.4	51.8	38	6	BD011790	BD011790 RNP deriv	C 171	11.2	50.0	40	9	S80703	S80703 Sequence
C 99	11.4	51.8	38	6	BD011791	BD011791 RNP deriv	C 172	11.2	50.0	40	9	S80703	S80703 Sequence
C 100	11.4	51.8	38	6	BD011791	BD011791 RNP deriv	C 173	11.2	50.0	42	6	AI6704	AI6704 Sequence
C 101	11.4	51.8	38	23	BD004187	BD004187 RNP deriv	C 174	11.2	50.0	43	6	AI6704	AI6704 Sequence
C 102	11.4	51.8	38	23	BD004187	BD004187 RNP deriv	C 175	11.2	50.0	43	6	AX002956	AX002956 Sequence
C 103	11.4	51.8	38	23	BD004188	BD004188 RNP deriv	C 176	11.2	50.0	43	6	AX002956	AX002956 Sequence
C 104	11.4	51.8	38	23	BD004188	BD004188 RNP deriv	C 177	11.2	50.0	46	6	AR082253	AR082253 Sequence
C 105	11.4	51.8	39	6	AR148967	AR148967 Sequence	C 178	11.2	50.0	46	6	AR082253	AR082253 Sequence
C 106	11.4	51.8	39	6	AR148967	AR148967 Sequence	C 179	11.2	50.0	46	6	AR082276	AR082276 Sequence
C 107	11.4	51.8	39	6	AR196819	AR196819 Sequence	C 180	11.2	50.0	46	6	AR082276	AR082276 Sequence
C 108	11.4	51.8	39	6	AR196819	AR196819 Sequence	C 181	11.2	50.0	46	6	AR120795	AR120795 Sequence
C 109	11.4	51.8	40	6	E04063	E04063 PCR primer.	C 182	11.2	50.0	46	6	AR120795	AR120795 Sequence
C 110	11.4	51.8	40	6	E04063	E04063 PCR primer.	C 183	11.2	50.0	46	6	AR120818	AR120818 Sequence
C 111	11.4	51.8	40	6	E04071	E04071 Primer for	C 184	11.2	50.0	46	6	AR120818	AR120818 Sequence
C 112	11.4	51.8	40	6	E04071	E04071 Primer for	C 185	11.2	50.0	46	6	I78289	I78289 Sequence
C 113	11.4	51.8	41	6	AR096162	AR096162 Sequence	C 186	11.2	50.0	46	6	I78289	I78289 Sequence
C 114	11.4	51.8	41	6	AR096162	AR096162 Sequence	C 187	11.2	50.0	46	6	I78322	I78322 Sequence
C 115	11.4	51.8	41	6	AR096163	AR096163 Sequence	C 188	11.2	50.0	46	6	I78322	I78322 Sequence
C 116	11.4	51.8	41	6	AR096163	AR096163 Sequence	C 189	11.2	50.0	48	6	AX224371	AX224371 Sequence
C 117	11.4	51.8	41	6	AR210561	AR210561 Sequence	C 190	11.2	50.0	48	6	AX224371	AX224371 Sequence
C 118	11.4	51.8	41	6	AR210561	AR210561 Sequence	C 191	11.2	50.0	48	6	I40773	I40773 Sequence
C 119	11.4	51.8	41	6	AR210562	AR210562 Sequence	C 192	11.2	50.0	48	6	I40773	I40773 Sequence
C 120	11.4	51.8	41	6	AR210562	AR210562 Sequence	C 193	10.8	49.1	20	6	AR067377	AR067377 Sequence
C 121	11.4	51.8	45	6	AX361281	AX361281 Sequence	C 194	10.8	49.1	20	6	AR067377	AR067377 Sequence
C 122	11.4	51.8	45	6	AX361281	AX361281 Sequence	C 195	10.8	49.1	22	6	A38334	A38334 Sequence 7
C 123	11.4	51.8	47	6	AR170381	AR170381 Sequence	C 196	10.8	49.1	22	6	A38334	A38334 Sequence 7
C 124	11.4	51.8	47	6	AR170381	AR170381 Sequence	C 197	10.8	49.1	26	6	AX481669	AX481669 Sequence
C 125	11.4	51.8	48	6	AR021432	AR021432 Sequence	C 198	10.8	49.1	26	6	AX481669	AX481669 Sequence
C 126	11.4	51.8	48	6	AR021432	AR021432 Sequence	C 199	10.8	49.1	28	6	AX57117	AX57117 Sequence
C 127	11.4	51.8	48	6	AR042994	AR042994 Sequence	C 200	10.8	49.1	28	6	AX57117	AX57117 Sequence
C 128	11.4	51.8	48	6	AR042994	AR042994 Sequence	C 201	10.8	49.1	28	6	AX57118	AX57118 Sequence
C 129	11.4	51.8	48	6	AR161328	AR161328 Sequence	C 202	10.8	49.1	28	6	AX57118	AX57118 Sequence
C 130	11.4	51.8	48	6	AR161328	AR161328 Sequence	C 203	10.8	49.1	28	6	AX153831	AX153831 Sequence
C 131	11.4	51.8	48	6	I43973	I43973 Sequence, 64	C 204	10.8	49.1	28	6	AX153831	AX153831 Sequence
C 132	11.4	51.8	48	6	I43973	I43973 Sequence, 64	C 205	10.8	49.1	29	6	A31175	A31175 DNA fragmen
C 133	11.4	51.8	48	6	I62985	I62985 Sequence 11	C 206	10.8	49.1	29	6	A31175	A31175 DNA fragmen
C 134	11.4	51.8	48	6	I62985	I62985 Sequence 11	C 207	10.8	49.1	34	6	AR091730	AR091730 Sequence
C 135	11.4	51.8	48	6	I62985	I62985 Sequence 11	C 208	10.8	49.1	34	6	AR091730	AR091730 Sequence
C 136	11.4	51.8	48	6	I88738	I88738 Sequence 11	C 209	10.8	49.1	40	6	AR069956	AR069956 Sequence
C 137	11.2	50.9	20	6	AX298397	AX298397 Sequence	C 210	10.8	49.1	40	6	AR069956	AR069956 Sequence
C 138	11.2	50.9	20	6	AX298397	AX298397 Sequence	C 211	10.8	49.1	40	6	AR076090	AR076090 Sequence

C 212	10.8	49.1	40	6	AR076090	AR076090 Sequence	285	10.6	48.2	25	6	E44264	E44264 Oligo-DNA s
C 213	10.8	49.1	40	6	BD007642	BD007642 Process f	C 286	10.6	48.2	25	6	E44264	E44264 Oligo-DNA s
C 214	10.8	49.1	40	6	BD007642	BD007642 Process f	C 287	10.6	48.2	26	6	BD000266	BD000266 Oligonuc1
C 215	10.8	49.1	41	6	AX113779	AX113779 Sequence	C 288	10.6	48.2	26	6	BD000266	BD000266 Oligonuc1
C 216	10.8	49.1	41	6	AX113779	AX113779 Sequence	C 289	10.6	48.2	27	6	AX036874	AX036874 Sequence
C 217	10.8	49.1	45	6	AJ3049	AJ3049 Id-phoA1a16	C 290	10.6	48.2	27	6	AX036874	AX036874 Sequence
C 218	10.8	49.1	45	6	AJ3049	AJ3049 Id-phoA1a16	C 291	10.6	48.2	27	6	AX083709	AX083709 Sequence
C 219	10.8	49.1	48	6	AR069955	AR069955 Sequence	C 292	10.6	48.2	27	6	AX083709	AX083709 Sequence
C 220	10.8	49.1	48	6	AR069955	AR069955 Sequence	C 293	10.6	48.2	29	6	AX253007	AX253007 Sequence
C 221	10.8	49.1	48	6	AR076089	AR076089 Sequence	C 294	10.6	48.2	29	6	AX253007	AX253007 Sequence
C 222	10.8	49.1	48	6	AR076089	AR076089 Sequence	C 295	10.6	48.2	30	6	A58136	A58136 Sequence 28
C 223	10.8	49.1	48	6	BD007641	BD007641 Process f	C 296	10.6	48.2	30	6	A58136	A58136 Sequence 28
C 224	10.8	49.1	50	6	BD007641	BD007641 Process f	C 297	10.6	48.2	30	6	BD012180	BD012180 Antineopl
C 225	10.8	49.1	50	6	AX093086	AX093086 Sequence	C 298	10.6	48.2	30	6	BD012180	BD012180 Antineopl
C 226	10.8	49.1	50	6	AX093086	AX093086 Sequence	C 299	10.6	48.2	30	6	E04686	E04686 Synthetic n
C 227	10.8	49.1	50	6	AX093090	AX093090 Sequence	C 300	10.6	48.2	30	6	E04686	E04686 Synthetic n
C 228	10.8	49.1	50	6	AX093090	AX093090 Sequence	C 301	10.6	48.2	30	23	BD004860	BD004860 Antineopl
C 229	10.6	48.2	18	6	A70959	A70959 Sequence 13	C 302	10.6	48.2	30	23	BD004860	BD004860 Antineopl
C 230	10.6	48.2	18	6	A70959	A70959 Sequence 13	C 303	10.6	48.2	31	6	AX480656	AX480656 Sequence
C 231	10.6	48.2	20	6	AR031036	AR031036 Sequence	C 304	10.6	48.2	31	6	AX480656	AX480656 Sequence
C 232	10.6	48.2	20	6	AR031036	AR031036 Sequence	C 305	10.6	48.2	31	6	AX480657	AX480657 Sequence
C 233	10.6	48.2	20	6	AR139569	AR139569 Sequence	C 306	10.6	48.2	31	6	AX480657	AX480657 Sequence
C 234	10.6	48.2	20	6	AR139569	AR139569 Sequence	C 307	10.6	48.2	31	6	E50123	E50123 Porous ho11
C 235	10.6	48.2	20	6	AR167032	AR167032 Sequence	C 308	10.6	48.2	31	6	E50123	E50123 Porous ho11
C 236	10.6	48.2	20	6	AR167032	AR167032 Sequence	C 309	10.6	48.2	32	6	AR212127	AR212127 Sequence
C 237	10.6	48.2	20	6	AR210687	AR210687 Sequence	C 310	10.6	48.2	32	6	AR212127	AR212127 Sequence
C 238	10.6	48.2	20	6	AR210687	AR210687 Sequence	C 311	10.6	48.2	34	6	AX282130	AX282130 Sequence
C 239	10.6	48.2	20	11	DOGC00607A	L77547 Caris fam1	C 312	10.6	48.2	34	6	AX282130	AX282130 Sequence
C 240	10.6	48.2	20	11	DOGC00607A	L77547 Caris fam1	C 313	10.6	48.2	34	6	AX282130	AX282130 Sequence
C 241	10.6	48.2	20	12	AB068715	AB068715 Synthet1c	C 314	10.6	48.2	34	6	AX282239	AX282239 Sequence
C 242	10.6	48.2	20	12	AB068715	AB068715 Synthet1c	C 315	10.6	48.2	34	6	AX282239	AX282239 Sequence
C 243	10.6	48.2	21	6	A68285	A68285 Sequence 6	C 316	10.6	48.2	34	6	AX322890	AX322890 Sequence
C 244	10.6	48.2	21	6	A68285	A68285 Sequence 6	C 317	10.6	48.2	34	6	AX322890	AX322890 Sequence
C 245	10.6	48.2	21	6	A68350	A68350 Sequence 9	C 318	10.6	48.2	36	6	A70977	A70977 Sequence 31
C 246	10.6	48.2	21	6	A68350	A68350 Sequence 9	C 319	10.6	48.2	36	6	A70977	A70977 Sequence 31
C 247	10.6	48.2	21	6	AR007281	AR007281 Sequence	C 320	10.6	48.2	37	6	AX002959	AX002959 Sequence
C 248	10.6	48.2	21	6	AR007281	AR007281 Sequence	C 321	10.6	48.2	37	6	AX002959	AX002959 Sequence
C 249	10.6	48.2	21	6	AR0662700	AR0662700 Sequence	C 322	10.6	48.2	37	6	AX135989	AX135989 Sequence
C 250	10.6	48.2	21	6	AR0662700	AR0662700 Sequence	C 323	10.6	48.2	37	6	AX135989	AX135989 Sequence
C 251	10.6	48.2	21	6	AR154843	AR154843 Sequence	C 324	10.6	48.2	37	6	AX136046	AX136046 Sequence
C 252	10.6	48.2	21	6	AR154843	AR154843 Sequence	C 325	10.6	48.2	37	6	BD006881	BD006881 Oligonuc1
C 253	10.6	48.2	21	6	AR170540	AR170540 Sequence	C 326	10.6	48.2	37	6	BD006881	BD006881 Oligonuc1
C 254	10.6	48.2	21	6	AR170540	AR170540 Sequence	C 327	10.6	48.2	37	6	E25770	E25770 Method for
C 255	10.6	48.2	21	6	AR170704	AR170704 Sequence	C 328	10.6	48.2	37	6	E25770	E25770 Method for
C 256	10.6	48.2	21	6	AR170704	AR170704 Sequence	C 329	10.6	48.2	37	9	AB055780	AB055780 Homo sapi
C 257	10.6	48.2	21	6	AR174772	AR174772 Sequence	C 330	10.6	48.2	37	9	AB055780	AB055780 Homo sapi
C 258	10.6	48.2	21	6	AR174772	AR174772 Sequence	C 331	10.6	48.2	38	6	AX218870	AX218870 Sequence
C 259	10.6	48.2	21	6	E65368	E65368 Genome DNA	C 332	10.6	48.2	38	6	AX218870	AX218870 Sequence
C 260	10.6	48.2	21	6	E65368	E65368 Genome DNA	C 333	10.6	48.2	38	6	AX423905	AX423905 Sequence
C 261	10.6	48.2	22	6	105640	105640 Sequence 13	C 334	10.6	48.2	38	6	AX423905	AX423905 Sequence
C 262	10.6	48.2	22	6	105640	105640 Sequence 13	C 335	10.6	48.2	38	6	AX423939	AX423939 Sequence
C 263	10.6	48.2	23	6	AX057257	AX057257 Sequence	C 336	10.6	48.2	38	6	AX423939	AX423939 Sequence
C 264	10.6	48.2	23	6	AX057257	AX057257 Sequence	C 337	10.6	48.2	38	6	114878	114878 Sequence 5
C 265	10.6	48.2	24	6	AR103724	AR103724 Sequence	C 338	10.6	48.2	38	6	114878	114878 Sequence 5
C 266	10.6	48.2	24	6	AR103724	AR103724 Sequence	C 339	10.6	48.2	38	6	192688	192688 Sequence 5
C 267	10.6	48.2	24	6	AR175413	AR175413 Sequence	C 340	10.6	48.2	38	6	192688	192688 Sequence 5
C 268	10.6	48.2	24	6	AR175413	AR175413 Sequence	C 341	10.6	48.2	39	6	A38384	A38384 Sequence 19
C 269	10.6	48.2	24	6	AX110657	AX110657 Sequence	C 342	10.6	48.2	39	6	A38384	A38384 Sequence 19
C 270	10.6	48.2	24	6	AX110657	AX110657 Sequence	C 343	10.6	48.2	39	6	AR117907	AR117907 Sequence
C 271	10.6	48.2	24	6	AX250662	AX250662 Sequence	C 344	10.6	48.2	39	6	AR117907	AR117907 Sequence
C 272	10.6	48.2	24	6	AX250662	AX250662 Sequence	C 345	10.6	48.2	39	6	174385	174385 Sequence 19
C 273	10.6	48.2	24	6	AX419900	AX419900 Sequence	C 346	10.6	48.2	39	6	174385	174385 Sequence 19
C 274	10.6	48.2	24	6	AX419900	AX419900 Sequence	C 347	10.6	48.2	40	9	S80741	S80741 gamma delta
C 275	10.6	48.2	24	6	AX444788	AX444788 Sequence	C 348	10.6	48.2	40	9	S80741	S80741 gamma delta
C 276	10.6	48.2	24	6	AX444788	AX444788 Sequence	C 349	10.6	48.2	42	6	AX033806	AX033806 Sequence
C 277	10.6	48.2	25	6	BD000246	BD000246 Oligonuc1	C 350	10.6	48.2	42	6	AX033806	AX033806 Sequence
C 278	10.6	48.2	25	6	BD000246	BD000246 Oligonuc1	C 351	10.6	48.2	45	6	AR168037	AR168037 Sequence
C 279	10.6	48.2	25	6	BD000255	BD000255 Oligonuc1	C 352	10.6	48.2	45	6	AR168037	AR168037 Sequence
C 280	10.6	48.2	25	6	BD000255	BD000255 Oligonuc1	C 353	10.6	48.2	45	6	AR204808	AR204808 Sequence
C 281	10.6	48.2	25	6	BD000264	BD000264 Oligonuc1	C 354	10.6	48.2	45	6	AR204808	AR204808 Sequence
C 282	10.6	48.2	25	6	BD000264	BD000264 Oligonuc1	C 355	10.6	48.2	47	6	AR179591	AR179591 Sequence
C 283	10.6	48.2	25	6	E44263	E44263 Oligo-DNA s	C 356	10.6	48.2	47	6	AR179591	AR179591 Sequence
C 284	10.6	48.2	25	6	E44263	E44263 Oligo-DNA s	C 357	10.6	48.2	48	6	AR076907	AR076907 Sequence

C 358	10.6	48.2	48	6	AR076907	AR076907 Sequence	C 431	10.4	47.3	24	6	AX355778	AX355778 Sequence
C 359	10.6	48.2	48	6	AR076912	AR076912 Sequence	C 432	10.4	47.3	24	6	AX355778	AX355778 Sequence
C 360	10.6	48.2	48	6	AR076912	AR076912 Sequence	C 433	10.4	47.3	24	6	AX447335	AX447335 Sequence
C 361	10.6	48.2	48	6	AR167298	AR167298 Sequence	C 434	10.4	47.3	24	6	AX447335	AX447335 Sequence
C 362	10.6	48.2	48	6	AR167298	AR167298 Sequence	C 435	10.4	47.3	26	6	AR090772	AR090772 Sequence
C 363	10.6	48.2	48	6	AR167303	AR167303 Sequence	C 436	10.4	47.3	26	6	AR090772	AR090772 Sequence
C 364	10.6	48.2	48	6	AR167303	AR167303 Sequence	C 437	10.4	47.3	26	6	AR197807	AR197807 Sequence
C 365	10.6	48.2	50	1	FVBFOXIF	M18010 Flavobacter	C 438	10.4	47.3	26	6	AR197807	AR197807 Sequence
C 366	10.6	48.2	50	1	FVBFOXIF	M18010 Flavobacter	C 439	10.4	47.3	26	6	AX463156	AX463156 Sequence
C 367	10.6	48.2	50	6	AR028065	AR028065 Sequence	C 440	10.4	47.3	26	6	AX463156	AX463156 Sequence
C 368	10.6	48.2	50	6	AR028065	AR028065 Sequence	C 441	10.4	47.3	27	6	AX115612	AX115612 Sequence
C 369	10.6	48.2	50	6	BD000119	BD000119 Nucleic a	C 442	10.4	47.3	27	6	AX115612	AX115612 Sequence
C 370	10.6	48.2	50	6	BD000119	BD000119 Nucleic a	C 443	10.4	47.3	28	6	AX115390	AX115390 Sequence
C 371	10.6	48.2	50	6	BD004784	BD004784 Method of	C 444	10.4	47.3	28	6	AX115390	AX115390 Sequence
C 372	10.6	48.2	50	6	BD004784	BD004784 Method of	C 445	10.4	47.3	28	6	AR006745	AR006745 Sequence
C 373	10.6	48.2	50	6	BD006778	BD006778 Method fo	C 446	10.4	47.3	29	6	AR006745	AR006745 Sequence
C 374	10.6	48.2	50	6	BD006778	BD006778 Method fo	C 447	10.4	47.3	29	6	AR032021	AR032021 Sequence
C 375	10.6	48.2	50	6	E44267	E44267 Oligo-DNA s	C 448	10.4	47.3	29	6	AR032021	AR032021 Sequence
C 376	10.6	48.2	50	6	E44267	E44267 Oligo-DNA s	C 449	10.4	47.3	29	6	AR038517	AR038517 Sequence
C 377	10.6	48.2	50	6	E44268	E44268 Oligo-DNA s	C 450	10.4	47.3	29	6	AR038517	AR038517 Sequence
C 378	10.6	48.2	50	6	E44268	E44268 Oligo-DNA s	C 451	10.4	47.3	29	6	AR050864	AR050864 Sequence
C 379	10.6	48.2	50	6	E44269	E44269 Oligo-DNA s	C 452	10.4	47.3	29	6	AR050864	AR050864 Sequence
C 380	10.6	48.2	50	6	E44269	E44269 Oligo-DNA s	C 453	10.4	47.3	29	6	AX319796	AX319796 Sequence
C 381	10.6	48.2	50	6	E50439	E50439 Method for	C 454	10.4	47.3	29	6	AX319796	AX319796 Sequence
C 382	10.6	48.2	50	6	E50439	E50439 Method for	C 455	10.4	47.3	29	6	E05890	E05890 Primer. 9/1
C 383	10.4	47.3	14	6	I06036	I06036 Sequence 5	C 456	10.4	47.3	29	6	E05890	E05890 Primer. 9/1
C 384	10.4	47.3	14	6	I06036	I06036 Sequence 5	C 457	10.4	47.3	29	6	E07921	E07921 Primer. 9/1
C 385	10.4	47.3	14	6	I06041	I06041 Sequence 10	C 458	10.4	47.3	29	6	E07921	E07921 Primer. 9/1
C 386	10.4	47.3	14	6	I06041	I06041 Sequence 10	C 459	10.4	47.3	30	6	AX007150	AX007150 Sequence
C 387	10.4	47.3	14	6	I06042	I06042 Sequence 11	C 460	10.4	47.3	30	6	AX007150	AX007150 Sequence
C 388	10.4	47.3	14	6	I06042	I06042 Sequence 11	C 461	10.4	47.3	30	6	AX008215	AX008215 Sequence
C 389	10.4	47.3	18	6	AR130097	AR130097 Sequence	C 462	10.4	47.3	30	6	AX008215	AX008215 Sequence
C 390	10.4	47.3	18	6	AR130097	AR130097 Sequence	C 463	10.4	47.3	31	6	A38545	A38545 Sequence 5
C 391	10.4	47.3	20	6	AR029388	AR029388 Sequence	C 464	10.4	47.3	31	6	A38545	A38545 Sequence 5
C 392	10.4	47.3	20	6	AR029388	AR029388 Sequence	C 465	10.4	47.3	31	6	A67246	A67246 Sequence 2
C 393	10.4	47.3	20	6	AX293756	AX293756 Sequence	C 466	10.4	47.3	31	6	A67246	A67246 Sequence 2
C 394	10.4	47.3	20	6	AX293756	AX293756 Sequence	C 467	10.4	47.3	31	6	A94762	A94762 Sequence 6
C 395	10.4	47.3	20	6	AX293909	AX293909 Sequence	C 468	10.4	47.3	31	6	A94762	A94762 Sequence 6
C 396	10.4	47.3	20	6	AX293909	AX293909 Sequence	C 469	10.4	47.3	31	6	AR013839	AR013839 Sequence
C 397	10.4	47.3	20	6	AX402157	AX402157 Sequence	C 470	10.4	47.3	31	6	AR013839	AR013839 Sequence
C 398	10.4	47.3	20	6	AX402157	AX402157 Sequence	C 471	10.4	47.3	31	6	AR033793	AR033793 Sequence
C 399	10.4	47.3	20	6	AX402158	AX402158 Sequence	C 472	10.4	47.3	31	6	AR033793	AR033793 Sequence
C 400	10.4	47.3	20	6	AX402158	AX402158 Sequence	C 473	10.4	47.3	31	6	AR042453	AR042453 Sequence
C 401	10.4	47.3	20	6	BD004094	BD004094 Apoptosis	C 474	10.4	47.3	31	6	AR042453	AR042453 Sequence
C 402	10.4	47.3	20	6	BD004094	BD004094 Apoptosis	C 475	10.4	47.3	31	6	AR058333	AR058333 Sequence
C 403	10.4	47.3	20	6	I17925	I17925 Sequence 5	C 476	10.4	47.3	31	6	AR058333	AR058333 Sequence
C 404	10.4	47.3	20	6	I17925	I17925 Sequence 5	C 477	10.4	47.3	31	6	AR088159	AR088159 Sequence
C 405	10.4	47.3	21	6	A22397	A22397 Oligonucleo	C 478	10.4	47.3	31	6	AR088159	AR088159 Sequence
C 406	10.4	47.3	21	6	A22397	A22397 Oligonucleo	C 479	10.4	47.3	31	6	AR131296	AR131296 Sequence
C 407	10.4	47.3	21	6	AX369420	AX369420 Sequence	C 480	10.4	47.3	31	6	AR131296	AR131296 Sequence
C 408	10.4	47.3	21	6	AX369420	AX369420 Sequence	C 481	10.4	47.3	31	6	AR173194	AR173194 Sequence
C 409	10.4	47.3	21	6	E04564	E04564 PCR primer	C 482	10.4	47.3	31	6	AR173194	AR173194 Sequence
C 410	10.4	47.3	21	6	E04564	E04564 PCR primer	C 483	10.4	47.3	31	6	BD002474	BD002474 Gene comp
C 411	10.4	47.3	21	6	E05239	E05239 Part of DNA	C 484	10.4	47.3	31	6	BD002474	BD002474 Gene comp
C 412	10.4	47.3	21	6	E05239	E05239 Part of DNA	C 485	10.4	47.3	33	6	AR171835	AR171835 Sequence
C 413	10.4	47.3	21	6	E05255	E05255 Primer for	C 486	10.4	47.3	33	6	AR171835	AR171835 Sequence
C 414	10.4	47.3	21	6	E05255	E05255 Primer for	C 487	10.4	47.3	33	6	AX148590	AX148590 Sequence
C 415	10.4	47.3	21	6	I22223	I22223 Sequence 4	C 488	10.4	47.3	33	6	AX148590	AX148590 Sequence
C 416	10.4	47.3	21	6	I22223	I22223 Sequence 4	C 489	10.4	47.3	33	6	I86950	I86950 Sequence 39
C 417	10.4	47.3	21	6	I22226	I22226 Sequence 7	C 490	10.4	47.3	33	6	I86950	I86950 Sequence 39
C 418	10.4	47.3	21	6	I22226	I22226 Sequence 7	C 491	10.4	47.3	33	6	I95606	I95606 Sequence 21
C 419	10.4	47.3	21	14	PPHSRPHRA	M64810 Human papil	C 492	10.4	47.3	33	6	I95606	I95606 Sequence 21
C 420	10.4	47.3	21	14	PPHSRPHRA	M64810 Human papil	C 493	10.4	47.3	35	6	A31401	A31401 Salt-HindII
C 421	10.4	47.3	22	6	AR127459	AR127459 Sequence	C 494	10.4	47.3	35	6	A31401	A31401 Salt-HindII
C 422	10.4	47.3	22	6	AR127459	AR127459 Sequence	C 495	10.4	47.3	35	6	A08036	A08036 Oligonucleo
C 423	10.4	47.3	23	6	AX082405	AX082405 Sequence	C 496	10.4	47.3	36	6	A08036	A08036 Oligonucleo
C 424	10.4	47.3	23	6	AX082405	AX082405 Sequence	C 497	10.4	47.3	36	6	A31402	A31402 Salt-HindII
C 425	10.4	47.3	24	6	AX104645	AX104645 Sequence	C 498	10.4	47.3	36	6	A31402	A31402 Salt-HindII
C 426	10.4	47.3	24	6	AX104645	AX104645 Sequence	C 499	10.4	47.3	36	6	AR034005	AR034005 Sequence
C 427	10.4	47.3	24	6	AX289123	AX289123 Sequence	C 500	10.4	47.3	36	6	AR034005	AR034005 Sequence
C 428	10.4	47.3	24	6	AX289123	AX289123 Sequence	C 501	10.4	47.3	36	6	AR124014	AR124014 Sequence
C 429	10.4	47.3	24	6	AX289276	AX289276 Sequence	C 502	10.4	47.3	36	6	AR124014	AR124014 Sequence
C 430	10.4	47.3	24	6	AX289276	AX289276 Sequence	C 503	10.4	47.3	37	6	I31696	I31696 Sequence 4

C 504	10.4	47.3	37	6	I31696	I31696 Sequence 4	577	10.2	46.4	24	6	AR162030	AR162030 Sequence
C 505	10.4	47.3	38	6	AX319802	AX319802 Sequence	C 578	10.2	46.4	24	6	AR162030	AR162030 Sequence
C 506	10.4	47.3	38	6	AX319802	AX319802 Sequence	C 579	10.2	46.4	24	6	AX289037	AX289037 Sequence
C 507	10.4	47.3	39	6	AR118505	AR118505 Sequence	C 580	10.2	46.4	24	6	AX289037	AX289037 Sequence
C 508	10.4	47.3	39	6	AR118505	AR118505 Sequence	C 581	10.2	46.4	24	6	AX289291	AX289291 Sequence
C 509	10.4	47.3	40	6	AR15559	AR15559 Sequence 1	C 582	10.2	46.4	24	6	AX289291	AX289291 Sequence
C 510	10.4	47.3	40	6	AR15559	AR15559 Sequence 1	C 583	10.2	46.4	24	6	AX289361	AX289361 Sequence
C 511	10.4	47.3	40	6	AR15560	AR15560 Sequence 1	C 584	10.2	46.4	24	6	AX289361	AX289361 Sequence
C 512	10.4	47.3	40	6	AR15560	AR15560 Sequence 1	C 585	10.2	46.4	24	6	AX290805	AX290805 Sequence
C 513	10.4	47.3	40	6	AR044603	AR044603 Sequence	C 586	10.2	46.4	24	6	AX290805	AX290805 Sequence
C 514	10.4	47.3	40	6	AR044603	AR044603 Sequence	C 587	10.2	46.4	24	6	AX292518	AX292518 Sequence
C 515	10.4	47.3	40	6	AX456282	AX456282 Sequence	C 588	10.2	46.4	24	6	AX292518	AX292518 Sequence
C 516	10.4	47.3	40	6	AX456282	AX456282 Sequence	C 589	10.2	46.4	24	6	AX292518	AX292518 Sequence
C 517	10.4	47.3	40	6	E05433	E05433 Oligonucleo	C 590	10.2	46.4	24	6	AX292871	AX292871 Sequence
C 518	10.4	47.3	40	6	E05433	E05433 Oligonucleo	C 591	10.2	46.4	24	6	AX292871	AX292871 Sequence
C 519	10.4	47.3	40	6	I13133	I13133 Sequence 12	C 592	10.2	46.4	24	6	I03297	I03297 Sequence 1
C 520	10.4	47.3	40	6	I13133	I13133 Sequence 12	C 593	10.2	46.4	24	6	AX477105	AX477105 Sequence
C 521	10.4	47.3	40	6	I36492	I36492 Sequence 12	C 594	10.2	46.4	26	6	AX477105	AX477105 Sequence
C 522	10.4	47.3	43	6	I36492	I36492 Sequence 12	C 595	10.2	46.4	27	6	I73504	I73504 Sequence 7
C 523	10.4	47.3	43	6	I78653	I78653 Sequence 8	C 596	10.2	46.4	27	6	I73504	I73504 Sequence 7
C 524	10.4	47.3	43	6	I78653	I78653 Sequence 8	C 597	10.2	46.4	28	6	AX060371	AX060371 Sequence
C 525	10.4	47.3	43	6	I78654	I78654 Sequence 9	C 598	10.2	46.4	28	6	AX060371	AX060371 Sequence
C 526	10.4	47.3	43	6	I78654	I78654 Sequence 9	C 599	10.2	46.4	28	6	AX085435	AX085435 Sequence
C 527	10.4	47.3	46	12	SYNBRWF	M94408 Artificial	C 600	10.2	46.4	28	6	AX085435	AX085435 Sequence
C 528	10.4	47.3	46	12	SYNBRWF	M94408 Artificial	C 601	10.2	46.4	28	6	AX085435	AX085435 Sequence
C 529	10.4	47.3	48	6	AR020972	AR020972 Sequence	C 602	10.2	46.4	28	6	AX202163	AX202163 Sequence
C 530	10.4	47.3	48	6	AR020972	AR020972 Sequence	C 603	10.2	46.4	29	6	AX202163	AX202163 Sequence
C 531	10.4	47.3	48	6	AR043387	AR043387 Sequence	C 604	10.2	46.4	29	6	AR151653	AR151653 Sequence
C 532	10.4	47.3	48	6	AR043387	AR043387 Sequence	C 605	10.2	46.4	29	6	AR151653	AR151653 Sequence
C 533	10.4	47.3	48	6	AR062302	AR062302 Sequence	C 606	10.2	46.4	30	6	A39579	A39579 Sequence 18
C 534	10.4	47.3	48	6	AR062302	AR062302 Sequence	C 607	10.2	46.4	30	6	A39579	A39579 Sequence 18
C 535	10.4	47.3	48	6	AR183761	AR183761 Sequence	C 608	10.2	46.4	30	6	A58134	A58134 Sequence 26
C 536	10.4	47.3	48	6	AR183761	AR183761 Sequence	C 609	10.2	46.4	30	6	A58134	A58134 Sequence 26
C 537	10.4	47.3	48	6	AX076971	AX076971 Sequence	C 610	10.2	46.4	30	6	A93166	A93166 Sequence 18
C 538	10.4	47.3	48	6	AX076971	AX076971 Sequence	C 611	10.2	46.4	30	6	A93166	A93166 Sequence 18
C 539	10.4	47.3	48	6	AX299782	AX299782 Sequence	C 612	10.2	46.4	30	6	AR082500	AR082500 Sequence
C 540	10.4	47.3	48	6	AX299782	AX299782 Sequence	C 613	10.2	46.4	30	6	AR082500	AR082500 Sequence
C 541	10.2	46.4	18	6	AX352188	AX352188 Sequence	C 614	10.2	46.4	30	6	AR159658	AR159658 Sequence
C 542	10.2	46.4	18	6	AX352188	AX352188 Sequence	C 615	10.2	46.4	30	6	AR159658	AR159658 Sequence
C 543	10.2	46.4	20	6	AR074417	AR074417 Sequence	C 616	10.2	46.4	30	6	AX036915	AX036915 Sequence
C 544	10.2	46.4	20	6	AR074417	AR074417 Sequence	C 617	10.2	46.4	30	6	AX036915	AX036915 Sequence
C 545	10.2	46.4	20	6	AR173216	AR173216 Sequence	C 618	10.2	46.4	30	6	AX306644	AX306644 Sequence
C 546	10.2	46.4	20	6	AR173216	AR173216 Sequence	C 619	10.2	46.4	30	6	AX306644	AX306644 Sequence
C 547	10.2	46.4	20	6	AR174795	AR174795 Sequence	C 620	10.2	46.4	33	6	AR004392	AR004392 Sequence
C 548	10.2	46.4	20	6	AR174795	AR174795 Sequence	C 621	10.2	46.4	33	6	AR004392	AR004392 Sequence
C 549	10.2	46.4	20	6	AX293994	AX293994 Sequence	C 622	10.2	46.4	33	6	AR064954	AR064954 Sequence
C 550	10.2	46.4	20	6	AX293994	AX293994 Sequence	C 623	10.2	46.4	33	6	AR064954	AR064954 Sequence
C 551	10.2	46.4	20	6	AX297151	AX297151 Sequence	C 624	10.2	46.4	33	6	AR097184	AR097184 Sequence
C 552	10.2	46.4	20	6	AX297151	AX297151 Sequence	C 625	10.2	46.4	33	6	AR130682	AR130682 Sequence
C 553	10.2	46.4	20	6	E05254	E05254 Primer for	C 626	10.2	46.4	33	6	AR130682	AR130682 Sequence
C 554	10.2	46.4	20	6	E05254	E05254 Primer for	C 627	10.2	46.4	33	6	AR172031	AR172031 Sequence
C 555	10.2	46.4	20	6	E11071	E11071 Primer. 9/1	C 628	10.2	46.4	33	6	AR172031	AR172031 Sequence
C 556	10.2	46.4	20	6	E11071	E11071 Primer. 9/1	C 629	10.2	46.4	33	6	I82867	I82867 Sequence 46
C 557	10.2	46.4	21	6	E05231	E05231 Part of DNA	C 630	10.2	46.4	33	6	I82867	I82867 Sequence 46
C 558	10.2	46.4	21	6	E05231	E05231 Part of DNA	C 631	10.2	46.4	36	6	I31693	I31693 Sequence 1
C 559	10.2	46.4	21	6	E05235	E05235 Part of DNA	C 632	10.2	46.4	36	6	I31693	I31693 Sequence 1
C 560	10.2	46.4	21	6	E05235	E05235 Part of DNA	C 633	10.2	46.4	36	6	I62073	I62073 Sequence 62
C 561	10.2	46.4	21	6	E06293	E06293 Primer. 9/1	C 634	10.2	46.4	36	6	I62073	I62073 Sequence 62
C 562	10.2	46.4	21	6	E06293	E06293 Primer. 9/1	C 635	10.2	46.4	36	6	I77522	I77522 Sequence 22
C 563	10.2	46.4	21	6	E06489	E06489 Primer. 9/1	C 636	10.2	46.4	36	6	I77522	I77522 Sequence 22
C 564	10.2	46.4	21	6	E06489	E06489 Primer. 9/1	C 637	10.2	46.4	36	6	I78056	I78056 Sequence 76
C 565	10.2	46.4	22	6	AX104783	AX104783 Sequence	C 638	10.2	46.4	36	6	I78056	I78056 Sequence 76
C 566	10.2	46.4	22	6	AX104783	AX104783 Sequence	C 639	10.2	46.4	37	6	AX107345	AX107345 Sequence
C 567	10.2	46.4	22	6	AX104853	AX104853 Sequence	C 640	10.2	46.4	37	6	AX107345	AX107345 Sequence
C 568	10.2	46.4	22	6	AX104853	AX104853 Sequence	C 641	10.2	46.4	38	6	AR046531	AR046531 Sequence
C 569	10.2	46.4	22	6	AX105128	AX105128 Sequence	C 642	10.2	46.4	38	6	AR046531	AR046531 Sequence
C 570	10.2	46.4	22	6	AX105128	AX105128 Sequence	C 643	10.2	46.4	38	6	AX036914	AX036914 Sequence
C 571	10.2	46.4	23	6	AR153842	AR153842 Sequence	C 644	10.2	46.4	38	6	AX036914	AX036914 Sequence
C 572	10.2	46.4	23	6	AR153842	AR153842 Sequence	C 645	10.2	46.4	38	6	AX201776	AX201776 Sequence
C 573	10.2	46.4	23	6	AX020841	AX020841 Sequence	C 646	10.2	46.4	38	6	AX201776	AX201776 Sequence
C 574	10.2	46.4	23	6	AX020841	AX020841 Sequence	C 647	10.2	46.4	38	6	AX218869	AX218869 Sequence
C 575	10.2	46.4	24	6	A41226	A41226 Sequence 10	C 648	10.2	46.4	38	6	AX218869	AX218869 Sequence
C 576	10.2	46.4	24	6	A41226	A41226 Sequence 10	C 649	10.2	46.4	38	6	AX273501	AX273501 Sequence

C 650	10.2	46.4	38	6	AX273501	723	10	45.5	24	6	AX444718	AX444718 Sequence
C 651	10.2	46.4	38	6	153583	C 724	10	45.5	24	6	AX444718	AX444718 Sequence
C 652	10.2	46.4	38	6	153583	C 725	10	45.5	24	6	124200	124200 Sequence 22
C 653	10.2	46.4	39	6	A11980	C 726	10	45.5	24	6	124200	124200 Sequence 22
C 654	10.2	46.4	39	6	A11980	C 727	10	45.5	25	6	AR034944	AR034944 Sequence
C 655	10.2	46.4	39	6	AR099751	C 728	10	45.5	25	6	AR034944	AR034944 Sequence
C 656	10.2	46.4	39	6	AR099751	C 729	10	45.5	25	6	AX196990	AX196990 Sequence
C 657	10.2	46.4	39	6	AR099751	C 730	10	45.5	25	6	AX196990	AX196990 Sequence
C 658	10.2	46.4	39	6	106676	C 731	10	45.5	25	6	AX448125	AX448125 Sequence
C 659	10.2	46.4	39	6	106676	C 732	10	45.5	25	6	AX448125	AX448125 Sequence
C 660	10.2	46.4	40	6	A66035	C 733	10	45.5	25	6	124207	124207 Sequence 29
C 661	10.2	46.4	40	6	AR154825	C 734	10	45.5	25	6	124207	124207 Sequence 29
C 662	10.2	46.4	40	6	AR154825	C 735	10	45.5	25	6	136774	136774 Sequence 18
C 663	10.2	46.4	41	6	AX046598	C 736	10	45.5	25	6	136774	136774 Sequence 18
C 664	10.2	46.4	41	6	AX046598	C 737	10	45.5	26	6	AR063839	AR063839 Sequence
C 665	10.2	46.4	42	6	AX015114	C 738	10	45.5	26	6	AR063839	AR063839 Sequence
C 666	10.2	46.4	42	6	AX015114	C 739	10	45.5	27	6	AR187867	AR187867 Sequence
C 667	10.2	46.4	42	6	AR008303	C 740	10	45.5	27	6	AR187867	AR187867 Sequence
C 668	10.2	46.4	43	6	AR008303	C 741	10	45.5	27	6	AR190887	AR190887 Sequence
C 669	10.2	46.4	43	6	AR037293	C 742	10	45.5	27	6	AR190887	AR190887 Sequence
C 670	10.2	46.4	43	6	AR037293	C 743	10	45.5	27	6	AR196638	AR196638 Sequence
C 671	10.2	46.4	43	6	AR052163	C 744	10	45.5	27	6	AR196638	AR196638 Sequence
C 672	10.2	46.4	43	6	AR052163	C 745	10	45.5	27	6	104705	104705 Sequence 29
C 673	10.2	46.4	44	6	AR009627	C 746	10	45.5	27	6	104705	104705 Sequence 29
C 674	10.2	46.4	44	6	AR009627	C 747	10	45.5	27	6	171983	171983 Sequence 19
C 675	10.2	46.4	48	6	A11979	C 748	10	45.5	27	6	171983	171983 Sequence 19
C 676	10.2	46.4	48	6	A11979	C 749	10	45.5	27	6	171984	171984 Sequence 20
C 677	10.2	46.4	48	6	AX221492	C 750	10	45.5	27	6	171984	171984 Sequence 20
C 678	10.2	46.4	48	6	AX221492	C 751	10	45.5	27	6	171986	171986 Sequence 22
C 679	10.2	46.4	50	6	AR032974	C 752	10	45.5	27	6	171986	171986 Sequence 22
C 680	10.2	46.4	50	6	AR032974	C 753	10	45.5	27	6	171986	171986 Sequence 22
C 681	10.2	46.4	50	6	AR209638	C 754	10	45.5	27	10	MUSTCGBQ	M55961 Mouse T-cell
C 682	10.2	46.4	50	6	AR209638	C 755	10	45.5	28	6	MUSTCGBQ	M55961 Mouse T-cell
C 683	10.2	46.4	50	6	AX395202	C 756	10	45.5	28	6	A64577	A64577 Sequence 4
C 684	10.2	46.4	50	6	AX395202	C 757	10	45.5	29	6	AR143240	AR143240 Sequence
C 685	10.2	46.4	50	6	129714	C 758	10	45.5	29	6	AR143240	AR143240 Sequence
C 686	10.2	46.4	50	6	129714	C 759	10	45.5	30	6	A87158	A87158 Sequence 18
C 687	10.2	46.4	50	6	191388	C 760	10	45.5	30	6	A87158	A87158 Sequence 18
C 688	10.2	46.4	50	6	191388	C 761	10	45.5	30	6	A92743	A92743 Sequence 15
C 689	10.2	46.4	50	10	MUSTSRE2	C 762	10	45.5	30	6	A92743	A92743 Sequence 15
C 690	10.2	46.4	50	10	MUSTSRE2	C 763	10	45.5	30	6	AR182013	AR182013 Sequence
C 691	10.2	45.5	18	4	DOG2159P01	C 764	10	45.5	30	6	AR182013	AR182013 Sequence
C 692	10.2	45.5	18	4	DOG2159P01	C 765	10	45.5	30	6	AX033571	AX033571 Sequence
C 693	10.2	45.5	18	6	AR165361	C 766	10	45.5	30	6	AX033571	AX033571 Sequence
C 694	10.2	45.5	18	6	AR165361	C 767	10	45.5	30	6	AX297512	AX297512 Sequence
C 695	10.2	45.5	19	6	A83664	C 768	10	45.5	30	6	AX297512	AX297512 Sequence
C 696	10.2	45.5	19	6	A83664	C 769	10	45.5	31	6	A13741	A13741 Sequence
C 697	10.2	45.5	19	6	AR164414	C 770	10	45.5	31	6	A13741	A13741 Sequence
C 698	10.2	45.5	19	6	AR164414	C 771	10	45.5	31	6	A13742	A13742 Sequence
C 699	10.2	45.5	19	6	AX132423	C 772	10	45.5	31	6	A13742	A13742 Sequence
C 700	10.2	45.5	19	6	AX132423	C 773	10	45.5	31	6	A87140	A87140 Sequence 50
C 701	10.2	45.5	19	6	AX132424	C 774	10	45.5	31	6	A87140	A87140 Sequence 50
C 702	10.2	45.5	19	6	AX132424	C 775	10	45.5	31	6	A87183	A87183 Sequence 18
C 703	10.2	45.5	20	6	AX278432	C 776	10	45.5	31	6	A87183	A87183 Sequence 18
C 704	10.2	45.5	20	6	AX278432	C 777	10	45.5	31	6	AR195894	AR195894 Sequence
C 705	10.2	45.5	23	6	AR174973	C 778	10	45.5	31	6	AR195894	AR195894 Sequence
C 706	10.2	45.5	23	6	AR174973	C 779	10	45.5	31	6	AR206394	AR206394 Sequence
C 707	10.2	45.5	23	6	AR208529	C 780	10	45.5	31	6	AR206394	AR206394 Sequence
C 708	10.2	45.5	23	6	AR208529	C 781	10	45.5	31	6	BD002551	BD002551 Gene comp
C 709	10.2	45.5	23	6	AX212875	C 782	10	45.5	31	6	BD002551	BD002551 Gene comp
C 710	10.2	45.5	23	6	AX212875	C 783	10	45.5	31	6	BD002552	BD002552 Gene comp
C 711	10.2	45.5	24	6	AR084189	C 784	10	45.5	31	6	BD002552	BD002552 Gene comp
C 712	10.2	45.5	24	6	AR084189	C 785	10	45.5	32	6	AR029677	AR029677 Sequence
C 713	10.2	45.5	24	6	AR126129	C 786	10	45.5	32	6	AR029677	AR029677 Sequence
C 714	10.2	45.5	24	6	AR126129	C 787	10	45.5	33	6	A36524	A36524 Sequence 65
C 715	10.2	45.5	24	6	AR208169	C 788	10	45.5	33	6	A36524	A36524 Sequence 65
C 716	10.2	45.5	24	6	AR208169	C 789	10	45.5	33	6	A36534	A36534 Sequence 75
C 717	10.2	45.5	24	6	AX007149	C 790	10	45.5	33	6	A36534	A36534 Sequence 75
C 718	10.2	45.5	24	6	AX007149	C 791	10	45.5	33	6	AR080157	AR080157 Sequence
C 719	10.2	45.5	24	6	AX008214	C 792	10	45.5	33	6	AR080157	AR080157 Sequence
C 720	10.2	45.5	24	6	AX008214	C 793	10	45.5	33	6	AR080167	AR080167 Sequence
C 721	10.2	45.5	24	6	AX443671	C 794	10	45.5	33	6	AR080167	AR080167 Sequence
C 722	10.2	45.5	24	6	AX443671	C 795	10	45.5	33	6	119751	119751 Sequence 7

C 796	10	45.5	33	6	119751	119751 Sequence 7	869	10	45.5	39	6	AR141025	AR141025 Sequence
C 797	10	45.5	33	9	S80708	S80708 gamma delta	C 870	10	45.5	39	6	AR141025	AR141025 Sequence
C 798	10	45.5	33	9	S80708	S80708 gamma delta	C 871	10	45.5	39	6	AX364607	AX364607 Sequence
C 799	10	45.5	34	6	AR153253	AR153253 Sequence	C 872	10	45.5	39	6	AX364607	AX364607 Sequence
C 800	10	45.5	34	6	AR153253	AR153253 Sequence	C 873	10	45.5	39	6	I20223	I20223 Sequence
C 801	10	45.5	34	6	AR163254	AR163254 Sequence	C 874	10	45.5	39	6	I20223	I20223 Sequence
C 802	10	45.5	34	6	AR163254	AR163254 Sequence	C 875	10	45.5	40	6	A87129	A87129 Sequence
C 803	10	45.5	34	6	AR210995	AR210995 Sequence	C 876	10	45.5	40	6	A87129	A87129 Sequence
C 804	10	45.5	34	6	AR210995	AR210995 Sequence	C 877	10	45.5	40	6	A87178	A87178 Sequence
C 805	10	45.5	34	6	I27333	I27333 Sequence 8	C 878	10	45.5	40	6	A87178	A87178 Sequence
C 806	10	45.5	34	6	I27333	I27333 Sequence 8	C 879	10	45.5	40	6	AR206383	AR206383 Sequence
C 807	10	45.5	35	6	AX468238	AX468238 Sequence	C 880	10	45.5	40	6	AR206383	AR206383 Sequence
C 808	10	45.5	35	6	AX468238	AX468238 Sequence	C 881	10	45.5	40	6	AX056701	AX056701 Sequence
C 809	10	45.5	36	6	A51534	A51534 Sequence 19	C 882	10	45.5	40	6	AX056701	AX056701 Sequence
C 810	10	45.5	36	6	A51534	A51534 Sequence 19	C 883	10	45.5	40	6	AX490799	AX490799 Sequence
C 811	10	45.5	36	6	A51562	A51562 Sequence 22	C 884	10	45.5	40	6	AX490799	AX490799 Sequence
C 812	10	45.5	36	6	A51562	A51562 Sequence 22	C 885	10	45.5	41	6	AX327045	AX327045 Sequence
C 813	10	45.5	36	6	A87816	A87816 Sequence 12	C 886	10	45.5	41	6	AX327045	AX327045 Sequence
C 814	10	45.5	36	6	A87816	A87816 Sequence 12	C 887	10	45.5	41	6	E09354	E09354 Linker. 9/1
C 815	10	45.5	36	6	A91148	A91148 Sequence 12	C 888	10	45.5	41	6	E09354	E09354 Linker. 9/1
C 816	10	45.5	36	6	A91148	A91148 Sequence 12	C 889	10	45.5	41	6	I19903	I19903 Sequence 27
C 817	10	45.5	36	6	AR084288	AR084288 Sequence	C 890	10	45.5	41	6	I19903	I19903 Sequence 27
C 818	10	45.5	36	6	AR084288	AR084288 Sequence	C 891	10	45.5	41	6	I28529	I28529 Sequence 11
C 819	10	45.5	36	6	AR119408	AR119408 Sequence	C 892	10	45.5	41	6	I28529	I28529 Sequence 11
C 820	10	45.5	36	6	AR119408	AR119408 Sequence	C 893	10	45.5	41	6	I40998	I40998 Sequence 27
C 821	10	45.5	36	6	AR173499	AR173499 Sequence	C 894	10	45.5	41	6	I40998	I40998 Sequence 27
C 822	10	45.5	36	6	AR173499	AR173499 Sequence	C 895	10	45.5	42	6	A42229	A42229 Sequence 17
C 823	10	45.5	36	6	I25805	I25805 Sequence 3	C 896	10	45.5	42	6	A42229	A42229 Sequence 17
C 824	10	45.5	36	6	I25805	I25805 Sequence 3	C 897	10	45.5	42	6	A84048	A84048 Sequence 35
C 825	10	45.5	36	6	I28496	I28496 Sequence 16	C 898	10	45.5	42	6	A84048	A84048 Sequence 35
C 826	10	45.5	36	6	I28496	I28496 Sequence 16	C 899	10	45.5	44	6	AR048165	AR048165 Sequence
C 827	10	45.5	36	6	I95566	I95566 Sequence 21	C 900	10	45.5	44	6	AR048165	AR048165 Sequence
C 828	10	45.5	36	6	I95566	I95566 Sequence 21	C 901	10	45.5	45	6	A13745	A13745 Oligonucleo
C 829	10	45.5	36	9	HUMTCGDGC	HUMTCGDGC	C 902	10	45.5	45	6	A13745	A13745 Oligonucleo
C 830	10	45.5	36	9	HUMTCGDGC	HUMTCGDGC	C 903	10	45.5	46	6	AX098392	AX098392 Sequence
C 831	10	45.5	37	6	A18680	A18680 Oligonucleo	C 904	10	45.5	46	6	AX098392	AX098392 Sequence
C 832	10	45.5	37	6	A18680	A18680 Oligonucleo	C 905	10	45.5	47	6	A16640	A16640 Nucleotide
C 833	10	45.5	37	6	AR183322	AR183322 Sequence	C 906	10	45.5	47	6	A16640	A16640 Nucleotide
C 834	10	45.5	37	6	AR183322	AR183322 Sequence	C 907	10	45.5	47	6	A16652	A16652 Nucleotide
C 835	10	45.5	37	6	AX049946	AX049946 Sequence	C 908	10	45.5	47	6	A16652	A16652 Nucleotide
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C 837	10	45.5	37	6	I82310	I82310 Sequence 1	C 910	10	45.5	47	6	E09353	E09353 Linker. 9/1
C 838	10	45.5	37	6	I82310	I82310 Sequence 1	C 911	10	45.5	47	6	I19902	I19902 Sequence 26
C 839	10	45.5	38	6	AX100313	AX100313 Sequence	C 912	10	45.5	47	6	I19902	I19902 Sequence 26
C 840	10	45.5	38	6	AX100313	AX100313 Sequence	C 913	10	45.5	47	6	I28528	I28528 Sequence 10
C 841	10	45.5	38	6	AX218405	AX218405 Sequence	C 914	10	45.5	47	6	I28528	I28528 Sequence 10
C 842	10	45.5	38	6	AX218405	AX218405 Sequence	C 915	10	45.5	47	6	I40997	I40997 Sequence 26
C 843	10	45.5	38	6	AX218522	AX218522 Sequence	C 916	10	45.5	47	6	I40997	I40997 Sequence 26
C 844	10	45.5	38	6	AX218522	AX218522 Sequence	C 917	10	45.5	48	6	A02326	A02326 Synthetic s
C 845	10	45.5	38	6	AX218807	AX218807 Sequence	C 918	10	45.5	48	6	A02326	A02326 Synthetic s
C 846	10	45.5	38	6	AX218807	AX218807 Sequence	C 919	10	45.5	48	6	AR044682	AR044682 Sequence
C 847	10	45.5	38	6	AX218985	AX218985 Sequence	C 920	10	45.5	48	6	AR044682	AR044682 Sequence
C 848	10	45.5	38	6	AX218985	AX218985 Sequence	C 921	10	45.5	49	6	A13744	A13744 Oligonucleo
C 849	10	45.5	38	6	AX222657	AX222657 Sequence	C 922	10	45.5	49	6	A13744	A13744 Oligonucleo
C 850	10	45.5	38	6	AX222657	AX222657 Sequence	C 923	10	44.5	14	6	I06039	I06039 Sequence 8
C 851	10	45.5	38	6	AX227960	AX227960 Sequence	C 924	10	44.5	14	6	I06039	I06039 Sequence 8
C 852	10	45.5	38	6	AX227960	AX227960 Sequence	C 925	10	44.5	18	6	AX352186	AX352186 Sequence
C 853	10	45.5	38	6	AX228049	AX228049 Sequence	C 926	10	44.5	18	6	AX352186	AX352186 Sequence
C 854	10	45.5	38	6	AX228049	AX228049 Sequence	C 927	10	44.5	18	6	AX352189	AX352189 Sequence
C 855	10	45.5	38	6	AX228148	AX228148 Sequence	C 928	10	44.5	18	6	AX352189	AX352189 Sequence
C 856	10	45.5	38	6	AX228148	AX228148 Sequence	C 929	10	44.5	18	6	AX352196	AX352196 Sequence
C 857	10	45.5	38	6	AX423900	AX423900 Sequence	C 930	10	44.5	18	6	AX352196	AX352196 Sequence
C 858	10	45.5	38	6	AX423900	AX423900 Sequence	C 931	10	44.5	18	6	I78188	I78188 Sequence 89
C 859	10	45.5	38	6	AX423982	AX423982 Sequence	C 932	10	44.5	18	6	I78188	I78188 Sequence 89
C 860	10	45.5	38	6	AX423982	AX423982 Sequence	C 933	10	44.5	20	6	A92150	A92150 Sequence 16
C 861	10	45.5	38	6	AX424058	AX424058 Sequence	C 934	10	44.5	20	6	A92150	A92150 Sequence 16
C 862	10	45.5	38	6	AX424058	AX424058 Sequence	C 935	10	44.5	20	6	AR024483	AR024483 Sequence
C 863	10	45.5	38	6	I06113	I06113 Sequence 3	C 936	10	44.5	20	6	AR024483	AR024483 Sequence
C 864	10	45.5	38	6	I06113	I06113 Sequence 3	C 937	10	44.5	20	6	AR074332	AR074332 Sequence
C 865	10	45.5	38	6	I24970	I24970 Sequence 10	C 938	10	44.5	20	6	AR074332	AR074332 Sequence
C 866	10	45.5	38	6	I24970	I24970 Sequence 10	C 939	10	44.5	20	6	AR157116	AR157116 Sequence
C 867	10	45.5	39	6	A77188	A77188 Sequence 16	C 940	10	44.5	20	6	AR157116	AR157116 Sequence
C 868	10	45.5	39	6	A77188	A77188 Sequence 16	C 941	10	44.5	20	6	AX032684	AX032684 Sequence

C 942	9.8	44.5	20	6	AX032684	AX032684 Sequence
C 943	9.8	44.5	20	6	AX188580	AX188580 Sequence
C 944	9.8	44.5	20	6	AX188580	AX188580 Sequence
C 945	9.8	44.5	20	6	AX224351	AX224351 Sequence
C 946	9.8	44.5	20	6	AX224351	AX224351 Sequence
C 947	9.8	44.5	20	6	AX412189	AX412189 Sequence
C 948	9.8	44.5	20	6	AX412189	AX412189 Sequence
C 950	9.8	44.5	20	6	EO4286	EO4286 DNA encodin
C 951	9.8	44.5	20	6	EO4286	EO4286 DNA encodin
C 952	9.8	44.5	20	6	EO4287	EO4297 DNA encodin
C 953	9.8	44.5	20	6	EO4297	EO4297 DNA encodin
C 954	9.8	44.5	20	6	E13183	E13183 PCR primer
C 955	9.8	44.5	20	6	E36655	E36655 PCR primer
C 956	9.8	44.5	20	6	E36655	E36655 DNA and pla
C 957	9.8	44.5	20	6	E36655	E36655 DNA and pla
C 958	9.8	44.5	20	6	E120435	E120435 Sequence 14
C 959	9.8	44.5	20	6	E120435	E120435 Sequence 14
C 960	9.8	44.5	20	6	E123918	E123918 Sequence 20
C 961	9.8	44.5	20	6	E123918	E123918 Sequence 20
C 962	9.8	44.5	21	6	AR163459	AR163459 Sequence
C 963	9.8	44.5	22	6	AR163459	AR163459 Sequence
C 964	9.8	44.5	22	6	AR171145	AR171145 Sequence
C 965	9.8	44.5	22	6	AR171145	AR171145 Sequence
C 966	9.8	44.5	22	6	AX068503	AX068503 Sequence
C 967	9.8	44.5	22	6	AX068503	AX068503 Sequence
C 968	9.8	44.5	23	6	AR063214	AR063214 Sequence
C 969	9.8	44.5	23	6	AR063214	AR063214 Sequence
C 970	9.8	44.5	23	6	AR139981	AR139981 Sequence
C 971	9.8	44.5	23	6	AR139981	AR139981 Sequence
C 972	9.8	44.5	23	6	AR140300	AR140300 Sequence
C 973	9.8	44.5	23	6	AR140300	AR140300 Sequence
C 974	9.8	44.5	23	6	AR140578	AR140578 Sequence
C 975	9.8	44.5	23	6	AR140578	AR140578 Sequence
C 976	9.8	44.5	23	6	AR143715	AR143715 Sequence
C 977	9.8	44.5	23	6	AR143715	AR143715 Sequence
C 978	9.8	44.5	23	6	AX195534	AX195534 Sequence
C 979	9.8	44.5	23	6	AX195534	AX195534 Sequence
C 980	9.8	44.5	23	6	AX451880	AX451880 Sequence
C 981	9.8	44.5	23	6	AX451880	AX451880 Sequence
C 982	9.8	44.5	23	6	BD008406	BD008406 Glyphosat
C 983	9.8	44.5	23	6	BD008406	BD008406 Glyphosat
C 984	9.8	44.5	24	6	AA1490	AA1490 Sequence 5
C 985	9.8	44.5	24	6	AA1490	AA1490 Sequence 5
C 986	9.8	44.5	24	6	A92194	A92194 Sequence 5
C 987	9.8	44.5	24	6	A92194	A92194 Sequence 28
C 988	9.8	44.5	24	6	AR035477	AR035477 Sequence
C 989	9.8	44.5	24	6	AR035477	AR035477 Sequence
C 990	9.8	44.5	24	6	AR171114	AR171114 Sequence
C 991	9.8	44.5	24	6	AR171114	AR171114 Sequence
C 992	9.8	44.5	24	6	AX015869	AX015869 Sequence
C 993	9.8	44.5	24	6	AX015869	AX015869 Sequence
C 994	9.8	44.5	24	6	AX068472	AX068472 Sequence
C 995	9.8	44.5	24	6	AX146804	AX146804 Sequence
C 996	9.8	44.5	24	6	AX146804	AX146804 Sequence
C 997	9.8	44.5	24	6	AX444183	AX444183 Sequence
C 998	9.8	44.5	24	6	AX444183	AX444183 Sequence
C 999	9.8	44.5	24	6	AX444667	AX444667 Sequence
C 1000	9.8	44.5	24	6	AX444667	AX444667 Sequence

ALIGNMENTS

RESULT		1	PAT 21-NOV--2001
AX295560			
LOCUS	AX295560	20 bp	DNA
DEFINITION	Sequence 7322 from Patent WO0175548.		linear
ACCESSION	AX295560		
VERSION	AX295560.1	GI:17057249	
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		

REFERENCE	ARTIFICIAL SEQUENCES
1	1
AUTHORS	Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE	Method of designing addressable array for detection of nucleic acid
JOURNAL	Sequence differences using ligase detection reaction
	Patent: WO 0179548-A 7322 25-OCT-2001;
	CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES	location/Qualifiers
source	1..20
	/organism="synthetic construct"
	/db_xref="taxon:32630"
	/note="Hypothetical Probe Sequence"
BASE COUNT	3 a 7 c 5 g 5 t
ORIGIN	
Query Match	60.9%; Score 13.4; DB 6; Length 20;
Best Local Similarity	93.3%; Pred. No. 1.6e+05;
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 CTGAGACCGATATCG 15
Db	19 CTGAGACCGATATCG 5
RESULT 2	
LOCUS	AX295560/ 20 bp DNA PAT 21-NOV-2001
DEFINITION	Sequence 7322 from Patent WO0179548.
ACCESSION	AX295560
VERSION	AX295560.1 GI:17057249
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	synthetic construct.
REFERENCE	1
AUTHORS	Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE	Method of designing addressable array for detection of nucleic acid
JOURNAL	Sequence differences using ligase detection reaction
	Patent: WO 0179548-A 7322 25-OCT-2001;
	CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES	location/Qualifiers
source	1..20
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	/db_xref="taxon:32630"
	/note="Hypothetical Probe Sequence"
BASE COUNT	3 a 7 c 5 g 5 t
ORIGIN	
Query Match	60.9%; Score 13.4; DB 6; Length 20;
Best Local Similarity	93.3%; Pred. No. 1.6e+05;
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 CTGAGACCGATATCG 15
Db	19 CTGAGACCGATATCG 5
RESULT 3	
LOCUS	AX290927 24 bp DNA PAT 21-NOV-2001
DEFINITION	Sequence 2689 from Patent WO0179548.
ACCESSION	AX290927
VERSION	AX290927.1 GI:17052610
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	synthetic construct.
REFERENCE	1
AUTHORS	Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE	Method of designing addressable array for detection of nucleic acid
JOURNAL	Sequence differences using ligase detection reaction
	Patent: WO 0179548-A 2689 25-OCT-2001;
	CORNELL RESEARCH FOUNDATION, INC. (US)

FEATURES
source Location/Qualifiers
1. .24
/organism="synthetic construct"
/db xref="taxon:32630"
/note="Hypothetical Probe Sequence"

BASE COUNT 3 a 8 c 6 g 7 t
ORIGIN

Query Match 60.9%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGATATCGGTCTCAG 22
1 |||||
5 CCATATCGGTCTCAG 19

Db

RESULT 4
AX290927/c AX290927 24 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 2689 from Patent WO0179548.
DEFINITION
ACCESSION AX290927
VERSION AX290927.1 GI:17052610
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
FEATURES
1 artificial sequences.

REFERENCE
AUTHORS Barany, F., Zivvi, M., Gerry, N. P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using 1ligase detection reaction
PATENT: WO 0179548-A 2689 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source Location/Qualifiers
1. .24
/organism="synthetic construct"
/db xref="taxon:32630"
/note="Hypothetical Probe Sequence"

BASE COUNT 3 a 8 c 6 g 7 t
ORIGIN

Query Match 60.9%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCG 15
1 |||||
19 CTGAGACCGATATCG 5

Db

RESULT 5
AR161400 AR161400 44 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 391 from patent US 6255458.
DEFINITION
ACCESSION AR161400
VERSION AR161400.1 GI:16227272
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
1 Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Lomberg, N. and Kay, R. M.
TITLE High affinity human antibodies and human antibodies against digoxin
JOURNAL Patent: US 6255458-A 391 03-JUL-2001;
LOCATION/Qualifiers
1. .44
/organism="unknown"

BASE COUNT 10 a 11 c 12 g 11 t
ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 44;
Best Local Similarity 76.2%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTCTCAG 22
1 |||||
9 TGAGACCGATATCGGTCTCAG 29

Db

RESULT 6
AR161400/c AR161400 44 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 391 from patent US 6255458.
DEFINITION
ACCESSION AR161400
VERSION AR161400.1 GI:16227272
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
1 Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Lomberg, N. and Kay, R. M.
TITLE High affinity human antibodies and human antibodies against digoxin
JOURNAL Patent: US 6255458-A 391 03-JUL-2001;
LOCATION/Qualifiers
1. .44
/organism="unknown"

BASE COUNT 10 a 11 c 12 g 11 t
ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 44;
Best Local Similarity 76.2%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCA 21
1 |||||
29 CTGAGACCGATATCGGTCTCA 9

Db

RESULT 7
AX292255 AX292255 24 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 4017 from Patent WO0179548.
DEFINITION
ACCESSION AX292255
VERSION AX292255.1 GI:17053938
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
FEATURES
1 artificial sequences.

REFERENCE
AUTHORS Barany, F., Zivvi, M., Gerry, N. P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using 1ligase detection reaction
PATENT: WO 0179548-A 4017 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source Location/Qualifiers
1. .24
/organism="synthetic construct"
/db xref="taxon:32630"
/note="Hypothetical Probe Sequence"

BASE COUNT 4 a 7 c 8 g 5 t
ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 24;
Best Local Similarity 78.9%; Pred. No. 3.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCT 19
1 |||||
6 CTGAGACCGATATCGGTCT 24

Db

RESULT 8
AX292255/c AX292255 24 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 4017 from Patent WO0179548.
DEFINITION
ACCESSION AX292255

VERSION AX292255.1 GI:17053938
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Barany, F., Zivyl, M., Gerry, N.P., Favis, R. and Kliman, R.
 TITLE Method of designing addressable array for detection of nucleic acid
 JOURNAL sequence differences using ligase detection reaction
 PATENT: WO 0179548-A 4017 25-OCT-2001;
 CORNELL RESEARCH FOUNDATION, INC. (US)
 FEATURES
 source 1. .24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"
 BASE COUNT 4 a 7 c 8 g 5 t
 ORIGIN
 Query Match 57.3%; Score 12.6; DB 6; Length 24;
 Best Local Similarity 78.9%; Pred. No. 3.8e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 AGACCGATATCGGTCTCAG 22
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 24 AGACCGGTATGGGTCCAG 6
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 RESULT 9
 AX189358
 LOCUS Sequence 15 from Patent WO0148244.
 DEFINITION AX189358
 ACCESSION AX189358
 VERSION AX189358.1 GI:15142870
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Casey, W.M., Chen, J.G., Colton, H.M., Taylor, D.G. and Weiner, M.P.
 TITLE Detection of single nucleotide polymorphisms
 JOURNAL Patent: WO 0148244-A 15 05-JUL-2001;
 GLAXO GROUP LIMITED (GB)
 FEATURES
 source 1. .25
 Location/Qualifiers
 BASE COUNT 5 a 8 c 9 g 3 t
 ORIGIN
 Query Match 57.3%; Score 12.6; DB 6; Length 25;
 Best Local Similarity 78.9%; Pred. No. 3.8e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GAGACCGATATCGGTCTCA 21
 ||||| ||||| |||||
 5 GATACCGATCTCGGGCGCA 23
 ||||| ||||| |||||
 RESULT 10
 AX189358
 LOCUS Sequence 15 from Patent WO0148244.
 DEFINITION AX189358
 ACCESSION AX189358
 VERSION AX189358.1 GI:15142870
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Casey, W.M., Chen, J.G., Colton, H.M., Taylor, D.G. and Weiner, M.P.
 TITLE Detection of single nucleotide polymorphisms
 JOURNAL Patent: WO 0148244-A 15 05-JUL-2001;

GLAXO GROUP LIMITED (GB)
 FEATURES
 source 1. .25
 Location/Qualifiers
 BASE COUNT 5 a 8 c 9 g 3 t
 ORIGIN
 Query Match 57.3%; Score 12.6; DB 6; Length 25;
 Best Local Similarity 78.9%; Pred. No. 3.8e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TGAGACCGATATCGGTCTC 20
 ||||| ||||| |||||
 23 TGCGCCGAGATCGGTATC 5
 ||||| ||||| |||||
 RESULT 11
 BD009441
 LOCUS Probes, methods and kits for detection and typing of Helicobacter
 DEFINITION pylori, nucleic acids in biological samples.
 ACCESSION BD009441
 VERSION BD009441.1 GI:18637814
 KEYWORDS JP 2001502536-A/33.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Quint, W. and Doorn, L.J.V.
 TITLE Probes, methods and kits for detection and typing of Helicobacter
 JOURNAL pylori, nucleic acids in biological samples
 PATENT: JP 2001502536-A 33 27-FEB-2001;
 INNOGENETICS NV, DDL BV
 COMMENT OS Unidentified.
 PN JP 2001502536-A/33
 PD 27-FEB-2001
 PF 10-OCT-1997 JP 1998518004
 PR 16-OCT-1996 EP 96870131.8
 PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
 PC C1201/68, C07K14/205, C12N15/11
 CC CC
 FH FH
 FT Key
 FT source 1. .21
 Location/Qualifiers
 FEATURES
 source 1. .21
 Location/Qualifiers
 BASE COUNT 9 a 3 c 5 g 2 t 2 others
 ORIGIN
 Query Match 56.4%; Score 12.4; DB 6; Length 21;
 Best Local Similarity 72.2%; Pred. No. 4.8e+05;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 AGACCGATATCGGTCTCA 21
 ||||| ||||| |||||
 1 AGACCGATTAATGKCTTA 18
 ||||| ||||| |||||
 RESULT 12
 BD009441/c
 LOCUS Probes, methods and kits for detection and typing of Helicobacter
 DEFINITION pylori, nucleic acids in biological samples.
 ACCESSION BD009441
 VERSION BD009441.1 GI:18637814
 KEYWORDS JP 2001502536-A/33.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 21)

AUTHORS Quint, W. and Doorn, L.J.V.
TITLE Probes, methods and kits for detection and typing of Helicobacter
JOURNAL pylori nucleic acids in biological samples
PATENT: JP 2001502536-A 33 27-FEB-2001;
COMMENT INNOVENTICS NV, DDL BV
OS Unidentified
PN JP 2001502536-A/33
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 JP 96870131.8
PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
PC C12Q1/68, C07K14/205, C12N15/11
CC
FH
FT
FT
Key Location/Qualifiers
source /organism='Unidentified'.
Location/Qualifiers
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/db_xref='taxon:32644'
BASE COUNT 9 a 3 c 5 g 2 t 2 others
ORIGIN
Query Match 56.4%; Score 12.4; DB 6; Length 21;
Best Local Similarity 72.2%; Pred. No. 4.8e+05;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAGCCGATATCGCTCT 19
Db 18 TTAGMCCRTATCGCTCT 1
RESULT 13
LOCUS 127040 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 61 from patent US 5563036.
ACCESSION 127040
VERSION 127040.1 GI:1817816
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Peterson, M.G., Baichwal, V.R. and Strulovici, B.
TITLE Transcription factor-DNA binding assay
JOURNAL Patent: US 5563036-A 61 08-OCT-1996;
FEATURES Location/Qualifiers
source 1. .30
/organism='unknown'
BASE COUNT 9 a 7 c 9 g 5 t
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Best Local Similarity 72.7%; Pred. No. 4.6e+05;
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QY 1 CTGAGCCGATATCGCTCTCAG 22
Db 5 CTGGTACCGAAGCGGTACCAG 26
RESULT 14
LOCUS 127040/c 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 61 from patent US 5563036.
ACCESSION 127040
VERSION 127040.1 GI:1817816
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Peterson, M.G., Baichwal, V.R. and Strulovici, B.

TITLE Transcription factor-DNA binding assay
JOURNAL Patent: US 5563036-A 61 08-OCT-1996;
FEATURES Location/Qualifiers
source 1. .30
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BASE COUNT 9 a 7 c 9 g 5 t
ORIGIN
Query Match 56.4%; Score 12.4; DB 6; Length 30;
Best Local Similarity 72.7%; Pred. No. 4.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CTGAGCCGATATCGCTCTCAG 22
Db 26 CTGGTACCGTTTCGCTACCAG 5
RESULT 15
LOCUS A41699 32 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 26 from Patent EP0630968.
ACCESSION A41699
VERSION A41699.1 GI:2297322
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Fritz, H., Hennecke, F. and Kolmar, H.
TITLE Genetic selection of proteins able to bind a ligand by
JOURNAL signal-transduction in a microorganism
PATENT: EP 0630968-A 26 28-DEC-1994;
COMMENT BEHRINGERwerke AG (DE)
Other publication JP 6343472 941220
Other publication AU 6461494 941215
Other publication CA 2125536 941211
Other publication DE 4319296 941215.
FEATURES Location/Qualifiers
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/db_xref='taxon:32644'
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Best Local Similarity 92.9%; Pred. No. 4.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 CGATATCGGTCTCA 21
Db 9 CGATATCGGTCTCA 22
RESULT 16
LOCUS A41699 32 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 26 from Patent EP0630968.
ACCESSION A41699
VERSION A41699.1 GI:2297322
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Fritz, H., Hennecke, F. and Kolmar, H.
TITLE Genetic selection of proteins able to bind a ligand by
JOURNAL signal-transduction in a microorganism
PATENT: EP 0630968-A 26 28-DEC-1994;
COMMENT BEHRINGERwerke AG (DE)
Other publication JP 6343472 941220
Other publication AU 6461494 941215
Other publication CA 2125536 941211
Other publication DE 4319296 941215.

FEATURES
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Location/Qualifiers
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BASE COUNT 7 a 12 c 5 g 8 t
ORIGIN

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Best Local Similarity 92.9%; Pred. No. 4.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCG 15
Db 22 TGAGAACGATATCG 9

RESULT 17
AX361282 45 bp DNA linear PAT 15-FEB-2002
LOCUS AX361282
DEFINITION Sequence 13 from Patent WO0208435.
ACCESSION AX361282
VERSION AX361282.1 GI:18693905
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Ertl,P.F., Gough,G.W. and Ring,C.J.
TITLE Codon-optimized papilloma virus sequences
JOURNAL Patent: WO 0208435-A 13 31-JAN-2002;
GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .45
Location/Qualifiers
/db_xref="taxon:32630"
/db_xref="Oligonucleotide linker"
BASE COUNT 8 a 15 c 14 g 8 t
ORIGIN

Query Match 56.4%; Score 12.4; DB 6; Length 45;
Best Local Similarity 72.7%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 19 CTGCTACCGATATCGTCTCAG 40

RESULT 18
AX361282 45 bp DNA linear PAT 15-FEB-2002
LOCUS AX361282
DEFINITION Sequence 13 from Patent WO0208435.
ACCESSION AX361282
VERSION AX361282.1 GI:18693905
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Ertl,P.F., Gough,G.W. and Ring,C.J.
TITLE Codon-optimized papilloma virus sequences
JOURNAL Patent: WO 0208435-A 13 31-JAN-2002;
GLAXO GROUP LIMITED (GB)
FEATURES
source 1. .45
Location/Qualifiers
/db_xref="taxon:32630"
/db_xref="Oligonucleotide linker"
BASE COUNT 8 a 15 c 14 g 8 t
ORIGIN

Query Match 56.4%; Score 12.4; DB 6; Length 45;
Best Local Similarity 72.7%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 40 CCGCTACCGATATCGTCTCAG 19

RESULT 19
AX047302 24 bp DNA linear PAT 15-DEC-2000
LOCUS AX047302
DEFINITION Sequence 16 from Patent WO0068374.
ACCESSION AX047302
VERSION AX047302.1 GI:11876573
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Heifetz,P.B., Patton,D.A., Levin,J.Z., Que,Q., de Haan,P.T. and
TITLE Regulation of viral gene expression
JOURNAL Patent: WO 0068374-A 16 16-NOV-2000;
Novartis AG (CH); Novartis-Erfindungen Verwaltungsgesellschaft
m.b.H. (AT)
FEATURES
source 1. .24
Location/Qualifiers
/db_xref="taxon:32630"
/db_xref="HINK284"
BASE COUNT 7 a 7 c 4 g 6 t
ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ACCGATATCGGTCCTCAG 22
Db 5 AACGATTCGGTCTCAG 21

RESULT 20
AX047302 24 bp DNA linear PAT 15-DEC-2000
LOCUS AX047302
DEFINITION Sequence 16 from Patent WO0068374.
ACCESSION AX047302
VERSION AX047302.1 GI:11876573
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Heifetz,P.B., Patton,D.A., Levin,J.Z., Que,Q., de Haan,P.T. and
TITLE Regulation of viral gene expression
JOURNAL Patent: WO 0068374-A 16 16-NOV-2000;
Novartis AG (CH); Novartis-Erfindungen Verwaltungsgesellschaft
m.b.H. (AT)
FEATURES
source 1. .24
Location/Qualifiers
/db_xref="taxon:32630"
/db_xref="HINK284"
BASE COUNT 7 a 7 c 4 g 6 t
ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGT 17
Db 21 CTGAGACCGATATCGTT 5

CC	anti-sense: No.	CC	anti-sense: No.
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
source	1..26	source	1..26
	/organism="synthetic construct"		/organism="synthetic construct"
	/db_xref="taxon:32630"		/db_xref="taxon:32630"
BASE COUNT	7 a 8 c 7 g 4 t	BASE COUNT	7 a 8 c 7 g 4 t
ORIGIN		ORIGIN	
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Best Local Similarity	82.4%; Pred. No. 5.8e+05;	Best Local Similarity	82.4%; Pred. No. 5.8e+05;
Matches	14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Matches	14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	6 ACCGATATCGGCTCCAG 22	OY	6 ACCGATATCGGCTCCAG 22
Db		Db	
	23 ACGATGTCCTCTCAG 7		23 ACGATGTCCTCTCAG 7
RESULT 23		RESULT 23	
E10842		E10842	
LOCUS	E10842 26 bp DNA linear PAT 29-SEP-1997	LOCUS	E10842 26 bp DNA linear PAT 29-SEP-1997
DEFINITION	PCR primer for detecting Hepatitis C virus.	DEFINITION	PCR primer for detecting Hepatitis C virus.
ACCESSION	E10842	ACCESSION	E10842
VERSION	E10842.1 GI:22027936	VERSION	E10842.1 GI:22027936
KEYWORDS	JP 1996056672-A/4.	KEYWORDS	JP 1996056672-A/4.
SOURCE	unidentified.	SOURCE	unidentified.
ORGANISM	unclassified.	ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 26)	REFERENCE	1 (bases 1 to 26)
AUTHORS	Chayama,K. and Kumada,H.	AUTHORS	Chayama,K. and Kumada,H.
TITLE	GENE OF TYPE C HEPATITIS VIRUS	TITLE	GENE OF TYPE C HEPATITIS VIRUS
JOURNAL	Patent: JP 1996056672-A 4 05-MAR-1996;	JOURNAL	Patent: JP 1996056672-A 4 05-MAR-1996;
COMMENT	CHAYAMA KAZUAKI	COMMENT	CHAYAMA KAZUAKI
	OS None		OS None
	OC Artificial sequences.		OC Artificial sequences.
	PN JP 1996056672-A/4		PN JP 1996056672-A/4
	PD 05-MAR-1996		PD 05-MAR-1996
	PF 26-AUG-1994 JP 199423393		PF 26-AUG-1994 JP 199423393
	PI CHAYAMA KAZUAKI, KUMADA HIROMITSU		PI CHAYAMA KAZUAKI, KUMADA HIROMITSU
	PC C12N15/09,A61K39/29,C07K14/18,C12N1/21,C12P21/02,C12Q1/68, PC		PC C12N15/09,A61K39/29,C07K14/18,C12N1/21,C12P21/02,C12Q1/68, PC
	GOINJ3/576,		GOINJ3/576,
	PC (C12N1/21,C12R1.91),(C12P21/02,C12R1.91);		PC (C12N1/21,C12R1.91),(C12P21/02,C12R1.91);
	CC strandedness: Single;		CC strandedness: Single;
	CC topology: Linear;		CC topology: Linear;
	CC hypothetical: No;		CC hypothetical: No;
	CC anti-sense: No;		CC anti-sense: No;
	FH Key		FH Key
	FT source		FT source
FEATURES	1..26	FEATURES	1..26
source	Location/Qualifiers	source	Location/Qualifiers
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	/organism="Artificial sequences"		/organism="Artificial sequences"
	/organism="unidentified"		/organism="unidentified"
	/db_xref="taxon:32644"		/db_xref="taxon:32644"
BASE COUNT	7 a 8 c 7 g 4 t	BASE COUNT	7 a 8 c 7 g 4 t
ORIGIN		ORIGIN	
Query Match	55.5%; Score 12.2; DB 6; Length 26;	Query Match	55.5%; Score 12.2; DB 6; Length 26;
Best Local Similarity	82.4%; Pred. No. 5.8e+05;	Best Local Similarity	82.4%; Pred. No. 5.8e+05;
Matches	14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Matches	14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	1 CTGAGACCGATTCGGT 17	OY	1 CTGAGACCGATTCGGT 17
Db		Db	
	7 CTGAGACCGACATCCGT 23		7 CTGAGACCGACATCCGT 23
RESULT 24		RESULT 24	
E10842/c		E10842/c	
LOCUS	E10842 26 bp DNA linear PAT 29-SEP-1997	LOCUS	E10842 26 bp DNA linear PAT 29-SEP-1997
DEFINITION	PCR primer for detecting Hepatitis C virus.	DEFINITION	PCR primer for detecting Hepatitis C virus.
ACCESSION	E10842	ACCESSION	E10842
VERSION	E10842.1 GI:22027936	VERSION	E10842.1 GI:22027936
KEYWORDS	JP 1996056672-A/4.	KEYWORDS	JP 1996056672-A/4.
SOURCE	unidentified.	SOURCE	unidentified.

ORGANISM						
unclassified.						
REFERENCE						
1 (bases 1 to 26)						
Chayama,K. and Kumada,H.						
GENE OF TYPE C HEPATITIS VIRUS						
TITLE						
CHAYAMA KAZUAKI						
JOURNAL						
Patent: JP 199605672-A 4 05-MAR-1996;						
COMMENT						
OS None						
OC Artificial sequences.						
PN JP 199605672-A/4						
PD 05-MAR-1996						
PF 26-AUG-1994 JP 1994223933						
PI CHAYAMA KAZUAKI, KUMADA HIROMITSU						
PC C12N1/5/09,A6K139/29,C07K14/18,C12N1/21.C12P21/02.C12Q1/68, PC						
G01N3/576,						
PC (C12N1/21,C12R1:91),(C12P21/02,C12R1:91);						
CC strandedness: Single;						
CC topology: Linear;						
CC hypothetical: No;						
CC anti-sense: No;						
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location/Qualifiers						
1..26 /organism="unidentified"						
/db_xref="taxon:32644"						
BASE COUNT						
ORIGIN						
7 a 8 c 7 g 4 t						
Query Match						
Best Local Similarity 55.5%; Score 12.2; DB 6; Length 26;						
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;						
OY	6	ACCGATATCGGTCTCAG	22			
Dd	23	ACGGATGTCGCTCTCAG	7			
RESULT 25						
LOCUS AR120578 33 bp DNA linear PAT 16-MAY-2001						
DEFINITION Sequence 8 from patent US 6159477.						
ACCESSION AR120578						
VERSION AR120578.1 GI:14104154						
KEYWORDS						
SOURCE						
ORGANISM						
Unknown.						
Unclassified.						
REFERENCE						
1 (bases 1 to 33)						
Audonnet,J.-C. and Baudy,P.						
AUTHORS Canine herpesvirus based recombinant live vaccine, in particular						
TITLE against canine distemper, rabies or the parainfluenza 2 virus						
PATENT: US 6159477-A 8 12-DEC-2000;						
JOURNAL						
FEATURES						
Location/Qualifiers						
source						
1..33 /organism="unknown"						
BASE COUNT						
ORIGIN						
8 a 9 c 10 g 6 t						
Query Match						
Best Local Similarity 55.5%; Score 12.2; DB 6; Length 33;						
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;						
OY	5	GACGATATCGGTCTCA	21			
Dd	17	GATCGATATCGGCCCA	33			
RESULT 26						
LOCUS AR120578/c 33 bp DNA linear PAT 16-MAY-2001						

DEFINITION	Sequence 8 from patent US 6159477.
ACCESSION	AR120578
VERSION	AR120578.1
KEYWORDS	GI:14104154
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 33)
TITLE	Audonnet,J.-C. and Baudu,P.
JOURNAL	Canine herpesvirus based recombinant live vaccine, in particular
FEATURES	against canine distemper, rabies or the parainfluenza 2 virus
source	Patent: US 6159477-A 8 12-DEC-2000;
	Location/Qualifiers
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	/organism="unknown"
BASE COUNT	8 a 9 c 10 g 6 t
ORIGIN	
Query Match	55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity	82.4%; Pred. No. 5.6e+05;
Matches	14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	2 TGAGACCGATATCGGTC 18
Db	33 TGGGCCCGATATCGATC 17
RESULT 27	
LOCUS	AR120579 33 bp DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 9 from patent US 6159477.
ACCESSION	AR120579
VERSION	AR120579.1
KEYWORDS	GI:14104155
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 33)
TITLE	Audonnet,J.-C. and Baudu,P.
JOURNAL	Canine herpesvirus based recombinant live vaccine, in particular
FEATURES	against canine distemper, rabies or the parainfluenza 2 virus
source	Patent: US 6159477-A 9 12-DEC-2000;
	Location/Qualifiers
	1..33
	/organism="unknown"
BASE COUNT	6 a 10 c 9 g 8 t
ORIGIN	
Query Match	55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity	82.4%; Pred. No. 5.6e+05;
Matches	14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	2 TGAGACCGATATCGGTC 18
Ddb	5 TGGGCCCGATATCGATC 21
RESULT 28	
LOCUS	AR120579 33 bp DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 9 from patent US 6159477.
ACCESSION	AR120579
VERSION	AR120579.1
KEYWORDS	GI:14104155
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 33)
TITLE	Audonnet,J.-C. and Baudu,P.
JOURNAL	Canine herpesvirus based recombinant live vaccine, in particular
FEATURES	against canine distemper, rabies or the parainfluenza 2 virus
Patent:	US 6159477-A 9 12-DEC-2000;
Location/Qualifiers	


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source      1..33              /organism="unknown"
BASE COUNT          6   a       10 c        9 g         8 t
ORIGIN

Query Match           55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 82.4%; Pred.No. 5.6e+05;
Matches    14; Conservative     0; Mismatches    3; Indels    0; Gaps    0;

QY
Db                5 GACCGATTCGGTCTCA 21
                  ||||| | | | | | | | |
                  21 GATCGATTCCGCCCCA 5

RESULT 29
LOCUS             I73498               33 bp DNA linear PAT 03-APR-1998
DEFINITION        Sequence 1 from patent US 5686579.
ACCESSION         I73498
VERSION           I73498.1 GI:3009639
KEYWORDS
SOURCE            unknown.
ORGANISM          Unclassified.
REFERENCE          1 (bases 1 to 33)
AUTHORS           Shami E.Y., Rothstein A. and Ramjeesingh.M.
TITLE             Use of antibody/antigen interactions to protect biologically active proteins and peptides Patent: US 5686579-A 1 11-NOV-1997; Location/Qualifiers
FEATURES          location=I73498
                    ..33
                    /organism="unknown"

BASE COUNT          6   a       9 c        6 g         5 t         7 others
ORIGIN

Query Match           55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 70.6%; Pred.No. 5.6e+05;
Matches    12; Conservative     3; Mismatches    2; Indels    0; Gaps    0;

QY
Db                5 GACCGATTCGGTCTCA 21
                  ||||| : | | | : | | |
                  5 GACCGAATYTGTGCTBA 21

RESULT 30
LOCUS             I73498/c             33 bp DNA linear PAT 03-APR-1998
DEFINITION        Sequence 1 from patent US 5686579.
ACCESSION         I73498
VERSION           I73498.1 GI:3009639
KEYWORDS
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE          1 (bases 1 to 33)
AUTHORS           Shami E.Y., Rothstein A. and Ramjeesinh,M.
TITLE             Use of antibody/antigen interactions to protect biologically active proteins and peptides Patent: US 5686579-A 1 11-NOV-1997; Location/Qualifiers
FEATURES          location=I73498/c
                    1..33
                    /organism="unknown"

BASE COUNT          6   a       9 c        6 g         5 t         7 others
ORIGIN

Query Match           55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 70.6%; Pred.No. 5.6e+05;
Matches    12; Conservative     3; Mismatches    2; Indels    0; Gaps    0;

QY
Db                2 TGAGCACCATTCCGTC 18
                  |:|:| |:|:| | | | | 
                  21 TVAGSACPATRITCGGTC 5

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[illegible]

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ACCESSION   AX138008
VERSION     AX138008.1  GI:14274103
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
            artificial sequences.
FEATURES
  source     1..37
             /organism="synthetic construct"
             /db_xref="taxon:32630"
             /note="primer"
             primer_bind
               1..37
               /note="Downstream primer"
BASE COUNT   16 a . 9 c 6 g 6 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 37;
Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
5 GACCGATATCGGTCCTCA 21
1 GATCGATATCTGTCTTA 17

RESULT 34
LOCUS       AX138008 37 bp. DNA linear PAT 30-MAY-2001
DEFINITION  Sequence 37 from Patent EP1083229.
ACCESSION   AX138008
VERSION     AX138008.1  GI:14274103
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
FEATURES
  source     1..37
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             /db_xref="taxon:32630"
             /note="primer"
             primer_bind
               1..37
               /note="Downstream primer"
BASE COUNT   16 a 9 c 6 g 6 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 37;
Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
2 TGAGACCGATATCGGTC 18
17 TTGACGATATCGATC 1

RESULT 35
LOCUS       ARI20598 39 bp. DNA linear PAT 16-MAY-2001
DEFINITION  Sequence 28 from patent US 6159477.
ACCESSION   ARI20598
VERSION     ARI20598.1  GI:14104174
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 39)
AUTHORS     Audonnet,J.-C. and Baudu,P.
TITLE       Canine herpesvirus based recombinant live vaccine, in particular
            against canine distemper, rabies or the parainfluenza 2 virus
JOURNAL     Patent: US 6159477-A 28 12-DEC-2000;
            Location/Qualifiers
            1..39
            /organism="unknown"
BASE COUNT   9 a 11 c 12 g 7 t
ORIGIN

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ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 39;
Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
5 GACCGATATCGGTCCTCA 21
23 GATCGATATCGGGCCCA 39

RESULT 36
LOCUS       ARI20598 39 bp. DNA linear PAT 16-MAY-2001
DEFINITION  Sequence 28 from patent US 6159477.
ACCESSION   ARI20598
VERSION     ARI20598.1  GI:14104174
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 39)
AUTHORS     Audonnet,J.-C. and Baudu,P.
TITLE       Canine herpesvirus based recombinant live vaccine, in particular
            against canine distemper, rabies or the parainfluenza 2 virus
JOURNAL     Patent: US 6159477-A 28 12-DEC-2000;
            Location/Qualifiers
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            /organism="unknown"
BASE COUNT   9 a 11 c 12 g 7 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 39;
Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
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5 TGGGCCCGATATCGATC 21

RESULT 37
LOCUS       ARI20599 39 bp. DNA linear PAT 16-MAY-2001
DEFINITION  Sequence 29 from patent US 6159477.
ACCESSION   ARI20599
VERSION     ARI20599.1  GI:14104175
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 39)
AUTHORS     Audonnet,J.-C. and Baudu,P.
TITLE       Canine herpesvirus based recombinant live vaccine, in particular
            against canine distemper, rabies or the parainfluenza 2 virus
JOURNAL     Patent: US 6159477-A 29 12-DEC-2000;
            Location/Qualifiers
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
2 TGAGACCGATATCGGTC 18
5 TGGGCCCGATATCGATC 21

RESULT 38
LOCUS       ARI20599/c

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LOCUS AR120599 39 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 29 from patent US 6159477.
 ACCESSION AR120599
 VERSION AR120599.1 GI:14104175
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 39)
 AUTHORS Audonnet,J.-C. and Baudu,P.
 TITLE Canine herpesvirus based recombinant live vaccine, in particular
 against canine distemper, rabies or the parainfluenza 2 virus
 JOURNAL Patent: US 6159477-A 29 12-DEC-2000;
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 BASE COUNT 7 a 12 c 11 g 9 t
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Query Match 55.5%; Score 12.2; DB 6; Length 39;
 Best Local Similarity 82.4%; Pred. No. 5.5e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GACCGATATCGGTCTCA 21
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 DB 21 GATCGATATCGGCGCCA 5

RESULT 39
 127047 127047 28 bp DNA linear PAT 06-FEB-1997
 LOCUS
 DEFINITION Sequence 68 from patent US 5563036.
 ACCESSION 127047
 VERSION 127047.1 GI:1817823
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Peterson,M.G., Baichwal,V.R. and Strulovici,B.
 TITLE Transcription factor-DNA binding assay
 JOURNAL Patent: US 5563036-A 68 08-OCT-1996;
 FEATURES
 source Location/Qualifiers
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BASE COUNT 9 a 7 c 9 g 3 t
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 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGGTCTCAG 22
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 DB 6 GTGACCGAAAAACGGTGTGAG 25

RESULT 40
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 LOCUS
 DEFINITION Sequence 68 from patent US 5563036.
 ACCESSION 127047
 VERSION 127047.1 GI:1817823
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Peterson,M.G., Baichwal,V.R. and Strulovici,B.
 TITLE Transcription factor-DNA binding assay
 JOURNAL Patent: US 5563036-A 68 08-OCT-1996;
 FEATURES
 source Location/Qualifiers
 1..28

BASE COUNT 9 a 7 c 9 g 3 t
 ORIGIN

Query Match 54.5%; Score 12; DB 6; Length 28;
 Best Local Similarity 75.0%; Pred. No. 7.1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 DB 25 CTCACACCGTTTTCGGTCA 6

Search completed: June 14, 2003, 22:14:56
 Job time : 1000 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 09:41:20 ; Search time 208 Seconds
(without alignments)
238.192 Million cell updates/sec

Title: US-09-532-001-1
Perfect score: 22
Sequence: 1 CTGAGACCGATATCGGTCTCAG 22

Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	22	100.0	22	19	AAV70907
4	14.2	64.5	28	21	AAV70834
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6	14	63.6	33	21	ABA98894
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8	14	63.6	40	21	AA295872
9	13.6	61.8	33	22	AAH46201

10	13.6	61.8	33	22	AAH46201	Hexapetaloid dupli
11	13.4	60.9	20	24	AB195602	Capture oligonucle
12	13.4	60.9	20	24	AB195602	Capture oligonucle
13	13.4	60.9	24	24	AB187774	Capture oligonucle
14	13.4	60.9	24	24	AB187774	Capture oligonucle
15	13.4	60.9	24	24	AB187775	Capture oligonucle
16	13.4	60.9	24	24	AB187775	Capture oligonucle
17	13	59.1	36	20	AAV04272	HAV-A linker regio
18	13	59.1	36	20	AAV04272	HAV-A linker regio
19	13	59.1	44	18	AAV78823	Kappa light chain
20	13	59.1	44	18	AAV78823	Kappa light chain
21	13	59.1	44	19	AAV39264	Primer o-561 used
22	13	59.1	44	19	AAV39264	Primer o-561 used
23	13	59.1	44	20	AA222018	Oligonucleotide us
24	13	59.1	44	20	AA222018	Oligonucleotide us
25	12.8	58.2	24	21	AA243102	PCR primer for C.
26	12.8	58.2	24	21	AA243102	PCR primer for C.
27	12.8	58.2	24	21	AA289641	Plasmid pUC19 prim
28	12.8	58.2	34	21	AA289641	Plasmid pUC19 prim
29	12.8	58.2	34	21	AA289642	Plasmid pUC19 prim
30	12.8	58.2	34	21	AA289642	Plasmid pUC19 prim
31	12.8	58.2	41	22	AA166435	Human thrombotic p
32	12.8	58.2	41	22	AA166435	Human thrombotic p
33	12.8	58.2	43	21	AA289643	Plasmid pUC19 prim
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35	12.8	58.2	43	21	AA289644	Plasmid pUC19 prim
36	12.8	58.2	43	21	AA289644	Plasmid pUC19 prim
37	12.6	57.3	24	24	AB190430	Capture oligonucle
38	12.6	57.3	24	24	AB190430	Capture oligonucle
39	12.6	57.3	24	24	AB190431	Capture oligonucle
40	12.6	57.3	24	24	AB190431	Capture oligonucle
41	12.6	57.3	25	22	AA210725	Myobacterium tube
42	12.6	57.3	25	22	AA210725	Myobacterium tube
43	12.4	56.4	20	20	AA205939	PCR primer used to
44	12.4	56.4	20	20	AA205939	PCR primer used to
45	12.4	56.4	21	19	AAV73540	H. pylori vacA pro
46	12.4	56.4	21	19	AAV73540	H. pylori vacA pro
47	12.4	56.4	32	16	AA080466	Primer (VUP2) com
48	12.4	56.4	32	16	AA080466	Primer (VUP2) com
49	12.2	55.5	21	22	AA096413	Human gene single
50	12.2	55.5	21	22	AA096413	Human gene single
51	12.2	55.5	24	22	AA02190	BNVV replicase ge
52	12.2	55.5	24	22	AA02190	BNVV replicase ge
53	12.2	55.5	26	15	AA05838	HCV detection prim
54	12.2	55.5	26	15	AA05838	HCV detection prim
55	12.2	55.5	26	15	AA05838	HCV detection prim
56	12.2	55.5	26	17	AA113284	Primer 1 for genom
57	12.2	55.5	26	17	AA113284	Primer 1 for genom
58	12.2	55.5	31	20	AAV83985	PCR primer C26 us
59	12.2	55.5	31	20	AAV83985	PCR primer C26 us
60	12.2	55.5	31	21	AA14934	PCR primer used to
61	12.2	55.5	31	21	AA14934	PCR primer used to
62	12.2	55.5	32	21	ABA98899	DNA sequence 7 rel
63	12.2	55.5	32	21	ABA98899	DNA sequence 7 rel
64	12.2	55.5	33	18	AAV66347	Light chain 5' sen
65	12.2	55.5	33	18	AAV66347	Light chain 5' sen
66	12.2	55.5	37	22	AA080208	PCR primer used to
67	12.2	55.5	37	22	AA080208	PCR primer used to
68	12.2	55.5	37	22	AA080208	PCR primer used to
69	12.2	55.5	37	22	AA080208	PCR primer used to
70	12.2	55.5	47	21	AA268554	Human map-related
71	12.2	55.5	47	21	AA268554	Human map-related
72	12	54.5	28	16	AA080343	The human papillom
73	12	54.5	28	16	AA080343	The human papillom
74	12	54.5	28	16	AA080344	Antisense oligonuc
75	12	54.5	28	16	AA080344	Antisense oligonuc
76	12	54.5	37	14	AA048276	Vbrioto proteolytic
77	12	54.5	37	14	AA048276	Vbrioto proteolytic
78	12	54.5	40	20	AA020311	PCR primer #43. S
79	12	54.5	40	20	AA020311	PCR primer #43. S
80	12	54.5	46	20	AA206995	Murine GABA B rece
81	12	54.5	46	20	AA206995	Murine GABA B rece
82	12	54.5	47	21	AA269147	Human map-related

83	11.8	53.6	24	24	ABL50125	Mouse telomerase c	156	11.4	51.8	40	14	AAO33059	PCR primer #6 used
84	11.8	53.6	24	24	ABL50125	Mouse telomerase c	157	11.4	51.8	40	14	AAO33438	Oligomer used in p
85	11.8	53.6	26	24	ABK49131	A. thaliana Activa	158	11.4	51.8	40	14	AAO33438	Oligomer used in p
86	11.8	53.6	26	24	ABK49131	A. thaliana Activa	159	11.4	51.8	40	16	AAT01323	Prepro-allymycin
87	11.8	53.6	29	24	ABK49135	A. thaliana Activa	160	11.4	51.8	40	16	AAT01323	Prepro-allymycin
88	11.8	53.6	29	24	ABK49135	A. thaliana Activa	161	11.4	51.8	41	24	ABK23971	Synthetic PCR prim
89	11.8	53.6	40	21	AAZ5959	Polynucleotide seq	162	11.4	51.8	41	24	ABK23971	Synthetic PCR prim
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91	11.8	53.6	45	16	AAO88181	Endonuclease r	164	11.4	51.8	41	24	ABK23972	Synthetic PCR prim
92	11.8	53.6	45	16	AAO88181	Endonuclease r	165	11.4	51.8	45	24	ABA95177	Linker used in the
93	11.6	52.7	19	21	AAZ75857	Human diallelic ma	166	11.4	51.8	45	24	ABA95177	Linker used in the
94	11.6	52.7	19	21	AAZ75857	Human diallelic ma	167	11.4	51.8	47	24	AAZ22537	Random RNA sequenc
95	11.6	52.7	20	20	AAZ06043	PCR primer used to	168	11.4	51.8	47	24	AAZ22537	Random RNA sequenc
96	11.6	52.7	20	20	AAZ06043	PCR primer used to	169	11.4	51.8	48	13	AAO22423	Human V kappa spec
97	11.6	52.7	21	19	AAV57628	Exon 13 of an ENAC	170	11.4	51.8	48	13	AAO22423	Human V kappa spec
98	11.6	52.7	21	19	AAV57628	Exon 13 of an ENAC	171	11.4	51.8	48	14	AAO44193	Probe Oligo-65 spe
99	11.6	52.7	21	20	AAV32063	MLH1 gene specific	172	11.4	51.8	48	14	AAO44193	Probe Oligo-65 spe
100	11.6	52.7	21	20	AAV32063	MLH1 gene specific	173	11.4	51.8	48	14	AAO50327	Human kappa light
101	11.6	52.7	30	24	ABK48802	Sau3AI adaptor Xs2	174	11.4	51.8	48	14	AAO50327	Human kappa light
102	11.6	52.7	30	24	ABK48802	Sau3AI adaptor Xs2	175	11.4	51.8	48	17	AAT37184	Human variable kap
103	11.6	52.7	38	22	AAH48754	Plasmid p35S-vacis	176	11.4	51.8	48	17	AAT37184	Human variable kap
104	11.6	52.7	38	22	AAH48754	Plasmid p35S-vacis	177	11.4	51.8	48	17	AAT37281	Human antibody kap
105	11.6	52.7	38	23	ABK04044	Human NOGO Hammer	178	11.4	51.8	48	17	AAT37281	Human antibody kap
106	11.6	52.7	38	23	ABK04044	Human NOGO Hammer	179	11.4	51.8	48	18	AAV12576	Probe Oligo-65 for
107	11.6	52.7	41	19	AAV39482	Haitpin oligonucle	180	11.4	51.8	48	18	AAV12576	Probe Oligo-65 for
108	11.6	52.7	41	19	AAV39482	Haitpin oligonucle	181	11.4	51.8	48	18	AAT70526	Human immunoglobul
109	11.6	52.7	47	21	AAZ69024	Human map-related	182	11.4	51.8	48	18	AAT70526	Human immunoglobul
110	11.6	52.7	47	21	AAZ69024	Human map-related	183	11.4	51.8	48	18	AAT73479	Human kappa light
111	11.4	51.8	18	16	AAO86666	NF-AT transcrip	184	11.4	51.8	48	18	AAT73479	Human kappa light
112	11.4	51.8	18	16	AAO86666	NF-AT transcrip	185	11.4	51.8	48	19	AAV38172	Probe Oligo-65 for
113	11.4	51.8	18	22	AAE31709	NF-AT-related prim	186	11.4	51.8	48	19	AAV38172	Probe Oligo-65 for
114	11.4	51.8	18	22	AAE31709	NF-AT-related prim	187	11.4	51.8	48	20	AAZ21964	Probe specific for
115	11.4	51.8	18	22	AAE31713	Human NF-ATc degen	188	11.4	51.8	48	20	AAZ21964	Probe specific for
116	11.4	51.8	18	22	AAE31713	Human NF-ATc degen	189	11.4	51.8	48	20	AAZ06048	Human kappa light
117	11.4	51.8	18	24	AAO34035	Reverse PCR primer	190	11.4	51.8	48	20	AAZ06048	Human kappa light
118	11.4	51.8	18	24	AAO34035	Reverse PCR primer	191	11.2	50.9	20	24	AAZ597421	Mutine SACT gene-s
119	11.4	51.8	20	24	ABN83710	Arthrobacter sp. d	192	11.2	50.9	20	24	AAZ597421	Mutine SACT gene-s
120	11.4	51.8	20	24	ABN83710	Arthrobacter sp. d	193	11.2	50.9	22	20	AAZ18134	GI tract binding p
121	11.4	51.8	25	21	AAZ55320	Mouse activation-i	194	11.2	50.9	22	20	AAZ18134	GI tract binding p
122	11.4	51.8	25	21	AAZ55320	Mouse activation-i	195	11.2	50.9	24	17	AAT30622	Probe nucleic acid
123	11.4	51.8	26	20	AAZ84133	PCR primer for Ara	196	11.2	50.9	24	17	AAT30622	Probe nucleic acid
124	11.4	51.8	26	20	AAZ84133	PCR primer for Ara	197	11.2	50.9	25	21	AAZ55301	Neisseria species
125	11.4	51.8	27	24	ABL41271	Diabody antibody r	198	11.2	50.9	25	21	AAZ55301	Neisseria species
126	11.4	51.8	27	24	ABL41271	Diabody antibody r	199	11.2	50.9	26	22	AAE17297	Information carryi
127	11.4	51.8	29	20	AAZ05577	Mab 96-110 variabl	200	11.2	50.9	26	22	AAE17297	Information carryi
128	11.4	51.8	29	20	AAZ05577	Mab 96-110 variabl	201	11.2	50.9	26	22	AAE17298	Information carryi
129	11.4	51.8	29	21	AAH11383	Tick-borne enceph	202	11.2	50.9	26	22	AAE17298	Information carryi
130	11.4	51.8	29	21	AAH11383	Tick-borne enceph	203	11.2	50.9	29	22	AAE84105	Yeast beta-type DN
131	11.4	51.8	29	22	AAZ10840	Human glucocerebro	204	11.2	50.9	29	22	AAE84105	Yeast beta-type DN
132	11.4	51.8	29	22	AAZ10840	Human glucocerebro	205	11.2	50.9	33	19	AAV49849	LM609 grafted anti
133	11.4	51.8	30	15	AAO74350	Human CD3 delta ch	206	11.2	50.9	33	19	AAV49849	LM609 grafted anti
134	11.4	51.8	30	15	AAO74350	Human CD3 delta ch	207	11.2	50.9	33	22	AAE28205	DNA encoding LM609
135	11.4	51.8	33	24	ABN81622	Fungal decaprenyl	208	11.2	50.9	33	22	AAE28205	DNA encoding LM609
136	11.4	51.8	33	24	ABN81622	Fungal decaprenyl	209	11.2	50.9	18	24	ABN86174	A. salmonicida str
137	11.4	51.8	34	21	AAZ52278	PCR1 forward prime	210	11.2	50.9	18	24	ABN86174	A. salmonicida str
138	11.4	51.8	34	21	AAZ52278	PCR1 forward prime	211	11.2	50.9	20	15	AAO55811	HCV detection prim
139	11.4	51.8	38	22	AAZ87445	Sendai virus NheI	212	11.2	50.9	20	15	AAO55811	HCV detection prim
140	11.4	51.8	38	22	AAZ87445	Sendai virus NheI	213	11.2	50.9	20	16	AAO80803	HCV genotype deter
141	11.4	51.8	38	22	AAZ87446	Sendai virus NheI	214	11.2	50.9	20	16	AAO80803	HCV genotype deter
142	11.4	51.8	38	22	AAZ87446	Sendai virus NheI	215	11.2	50.9	20	19	AAV69670	PRPR gene specific
143	11.4	51.8	38	22	AAZ87446	Sendai virus NheI	216	11.2	50.9	20	19	AAV69670	PRPR gene specific
144	11.4	51.8	38	22	AAZ87497	Sendai virus NheI	217	11.2	50.9	20	19	AAV37823	Human hepatitis vi
145	11.4	51.8	38	22	AAZ87497	Sendai virus NheI	218	11.2	50.9	20	19	AAV37823	Human hepatitis vi
146	11.4	51.8	38	22	AAZ87498	Sendai virus NheI	219	11.2	50.9	23	22	AAH76084	Rat CAR DNA amplif
147	11.4	51.8	38	22	AAZ87498	Sendai virus NheI	220	11.2	50.9	23	22	AAH76084	Rat CAR DNA amplif
148	11.4	51.8	38	24	AAZ33982	Sense primer #2 us	221	11.2	50.9	25	21	AAZ39008	Brevibacterium fla
149	11.4	51.8	38	24	AAZ33982	Sense primer #2 us	222	11.2	50.9	25	21	AAZ39008	Brevibacterium fla
150	11.4	51.8	38	24	AAZ33983	Antisense primer #	223	11.2	50.9	25	21	AAZ39008	Brevibacterium fla
151	11.4	51.8	39	20	AAZ37578	Human papilloma vi	224	11.2	50.9	25	21	AAZ37578	Human papilloma vi
152	11.4	51.8	39	20	AAZ37578	Human papilloma vi	225	11.2	50.9	25	24	ABO12058	Oligonucleotide ad
153	11.4	51.8	39	21	AAZ48186	HPV 16 LI expressi	226	11.2	50.9	25	24	ABO12058	Oligonucleotide ad
154	11.4	51.8	39	21	AAZ48186	HPV 16 LI expressi	227	11.2	50.9	26	22	AAH01449	blapR-1 resistanc
155	11.4	51.8	40	14	AAO33059	PCR primer #6 used	228	11.2	50.9	26	22	AAH01449	blapR-1 resistanc

229	11	50.0	30	21	AA295613	Oligonucleotide M-	C 302	10.8	49.1	41	22	AAF82655	Human ARE ITA int
C 230	11	50.0	30	21	AA295613	Oligonucleotide M-	C 303	10.8	49.1	41	24	ABL53552	Human chemokine LP
C 231	11	50.0	30	22	AA295640	Human CON202 G pro	C 304	10.8	49.1	41	24	ABL53552	Human chemokine LP
C 232	11	50.0	30	22	AA295640	Human CON202 G pro	C 305	10.8	49.1	45	13	AA023469	3' end of PCR-amp1
C 233	11	50.0	32	10	AA292279	Probe for 21 bp mo	C 306	10.8	49.1	45	13	AA023469	3' end of PCR-amp1
C 234	11	50.0	32	10	AA292279	Probe for 21 bp mo	C 307	10.8	49.1	47	15	AA044966	FelV gag/prot gene
C 235	11	50.0	32	18	AA295766	c-Ki-ras antisense	C 308	10.8	49.1	47	15	AA044966	FelV gag/prot gene
C 236	11	50.0	32	18	AA295766	c-Ki-ras antisense	C 309	10.8	49.1	47	20	AA295253	Human genome biall1
C 237	11	50.0	32	21	AA15021	PCR primer used to	C 310	10.8	49.1	47	20	AA295253	Human genome biall1
C 238	11	50.0	32	21	AA15021	PCR primer used to	C 311	10.8	49.1	47	21	AA265902	Human map-related
C 239	11	50.0	33	10	AA292277	Probe for 21 bp mo	C 312	10.8	49.1	47	21	AA265902	Human map-related
C 240	11	50.0	33	10	AA292277	Probe for 21 bp mo	C 313	10.8	49.1	47	21	AA267010	Human map-related
C 241	11	50.0	34	24	ABK88062	Biomembrane permea	C 314	10.8	49.1	47	21	AA267010	Human map-related
C 242	11	50.0	34	24	ABK88062	Biomembrane permea	C 315	10.8	49.1	48	21	AA289314	Hpv 83 ori DNA fra
C 243	11	50.0	36	14	AA048273	Vibrio campbellii	C 316	10.8	49.1	48	21	AA289314	Hpv 83 ori DNA fra
C 244	11	50.0	36	14	AA048273	Vibrio campbellii	C 317	10.8	49.1	49	21	AA229386	PCR primer-12 for
C 245	11	50.0	36	24	AA29711	Human BRCA1 gene a	C 318	10.8	49.1	49	21	AA229386	PCR primer-12 for
C 246	11	50.0	36	24	AA29711	Human BRCA1 gene a	C 319	10.8	49.1	50	21	AA229386	PCR primer-12 for
C 247	11	50.0	37	20	AA291965	Porphyromonas ging	C 320	10.8	49.1	50	22	AA291965	1467-00 PCR primer
C 248	11	50.0	37	20	AA291965	Porphyromonas ging	C 321	10.8	49.1	50	22	AA291965	1467-00 PCR primer
C 249	11	50.0	37	22	AA291965	Linker oligonucleo	C 322	10.8	49.1	50	22	AA291965	1467-04 oligonucle
C 250	11	50.0	37	22	AA291965	Linker oligonucleo	C 323	10.8	49.1	50	22	AA291965	1467-04 oligonucle
C 251	11	50.0	37	24	ABK47047	Adenovirus adapter	C 324	10.8	49.1	50	24	ABK47047	Treponema pallidum
C 252	11	50.0	37	24	ABK47047	Adenovirus adapter	C 325	10.8	49.1	50	24	ABK47047	Treponema pallidum
C 253	11	50.0	40	18	AA291965	Path-starting PCR	C 326	10.8	49.1	50	24	ABK47047	Treponema pallidum
C 254	11	50.0	40	18	AA291965	Path-starting PCR	C 327	10.8	49.1	17	21	AA291965	Microsatellite rep
C 255	11	50.0	43	20	AA291965	Pseudomonas sp. st	C 328	10.6	48.2	17	21	AA291965	Microsatellite rep
C 256	11	50.0	43	20	AA291965	Pseudomonas sp. st	C 329	10.6	48.2	18	19	AA291965	Microsatellite rep
C 257	11	50.0	43	21	AA291965	Pseudomonas sp. st	C 330	10.6	48.2	18	19	AA291965	Microsatellite rep
C 258	11	50.0	43	21	AA291965	Pseudomonas sp. st	C 331	10.6	48.2	18	19	AA291965	Microsatellite rep
C 259	11	50.0	43	21	AA291965	Pseudomonas sp. st	C 332	10.6	48.2	18	21	AA291965	Microsatellite rep
C 260	11	50.0	43	21	AA291965	Pseudomonas sp. st	C 333	10.6	48.2	20	13	AA291965	Microsatellite rep
C 261	11	50.0	46	16	AA083070	HIV hammerhead mot	C 334	10.6	48.2	20	13	AA291965	Microsatellite rep
C 262	11	50.0	46	16	AA083070	HIV hammerhead mot	C 335	10.6	48.2	20	15	AA057827	Primer pair 8A CST
C 263	11	50.0	46	16	AA083070	HIV hammerhead mot	C 336	10.6	48.2	20	15	AA057827	Primer pair 8A CST
C 264	11	50.0	46	16	AA083070	HIV hammerhead mot	C 337	10.6	48.2	20	15	AA057827	Primer pair 8A CST
C 265	11	50.0	47	21	AA267760	Human map-related	C 338	10.6	48.2	20	15	AA058411	Antisense oligonuc
C 266	11	50.0	47	21	AA267760	Human map-related	C 339	10.6	48.2	20	17	AA267760	Antisense oligonuc
C 267	11	50.0	48	17	AA267760	Human map-related	C 340	10.6	48.2	20	17	AA267760	Antisense oligonuc
C 268	11	50.0	48	17	AA267760	Human map-related	C 341	10.6	48.2	20	21	AA267760	Antisense oligonuc
C 269	11	50.0	48	22	AA267760	Human map-related	C 342	10.6	48.2	20	21	AA267760	Antisense oligonuc
C 270	11	50.0	48	22	AA267760	Human map-related	C 343	10.6	48.2	20	21	AA267760	Antisense oligonuc
C 271	11	50.0	48	22	AA267760	Human map-related	C 344	10.6	48.2	20	21	AA267760	Antisense oligonuc
C 272	11	50.0	48	22	AA267760	Human map-related	C 345	10.6	48.2	20	24	AB144258	Human chromosome 1
C 273	11	50.0	50	20	AA222993	5' primer used for	C 346	10.6	48.2	20	24	AB144258	Human chromosome 1
C 274	11	50.0	50	20	AA222993	5' primer used for	C 347	10.6	48.2	21	17	AA222993	Human chromosome 1
C 275	10.8	49.1	50	20	AA222993	5' primer used for	C 348	10.6	48.2	21	17	AA222993	Human chromosome 1
C 276	10.8	49.1	50	20	AA222993	5' primer used for	C 349	10.6	48.2	21	19	AA222993	Human chromosome 1
C 277	10.8	49.1	50	20	AA222993	5' primer used for	C 350	10.6	48.2	21	19	AA222993	Human chromosome 1
C 278	10.8	49.1	50	20	AA222993	5' primer used for	C 351	10.6	48.2	21	19	AA222993	Human chromosome 1
C 279	10.8	49.1	50	20	AA222993	5' primer used for	C 352	10.6	48.2	21	21	AA222993	Human chromosome 1
C 280	10.8	49.1	50	20	AA222993	5' primer used for	C 353	10.6	48.2	21	21	AA222993	Human chromosome 1
C 281	10.8	49.1	50	20	AA222993	5' primer used for	C 354	10.6	48.2	21	21	AA222993	Human chromosome 1
C 282	10.8	49.1	50	20	AA222993	5' primer used for	C 355	10.6	48.2	21	22	AA222993	Human chromosome 1
C 283	10.8	49.1	50	20	AA222993	5' primer used for	C 356	10.6	48.2	21	22	AA222993	Human chromosome 1
C 284	10.8	49.1	50	20	AA222993	5' primer used for	C 357	10.6	48.2	21	22	AA222993	Human chromosome 1
C 285	10.8	49.1	50	20	AA222993	5' primer used for	C 358	10.6	48.2	21	23	AA222993	Human chromosome 1
C 286	10.8	49.1	50	20	AA222993	5' primer used for	C 359	10.6	48.2	21	23	AA222993	Human chromosome 1
C 287	10.8	49.1	50	20	AA222993	5' primer used for	C 360	10.6	48.2	21	24	AA222993	Human chromosome 1
C 288	10.8	49.1	50	20	AA222993	5' primer used for	C 361	10.6	48.2	21	24	AA222993	Human chromosome 1
C 289	10.8	49.1	50	20	AA222993	5' primer used for	C 362	10.6	48.2	21	24	AA222993	Human chromosome 1
C 290	10.8	49.1	50	20	AA222993	5' primer used for	C 363	10.6	48.2	22	21	AA222993	Human chromosome 1
C 291	10.8	49.1	50	20	AA222993	5' primer used for	C 364	10.6	48.2	22	21	AA222993	Human chromosome 1
C 292	10.8	49.1	50	20	AA222993	5' primer used for	C 365	10.6	48.2	22	22	AA222993	Human chromosome 1
C 293	10.8	49.1	50	20	AA222993	5' primer used for	C 366	10.6	48.2	22	22	AA222993	Human chromosome 1
C 294	10.8	49.1	50	20	AA222993	5' primer used for	C 367	10.6	48.2	22	24	AA222993	Human chromosome 1
C 295	10.8	49.1	50	20	AA222993	5' primer used for	C 368	10.6	48.2	22	24	AA222993	Human chromosome 1
C 296	10.8	49.1	50	20	AA222993	5' primer used for	C 369	10.6	48.2	22	24	AA222993	Human chromosome 1
C 297	10.8	49.1	50	20	AA222993	5' primer used for	C 370	10.6	48.2	23	21	AA222993	Human chromosome 1
C 298	10.8	49.1	50	20	AA222993	5' primer used for	C 371	10.6	48.2	23	21	AA222993	Human chromosome 1
C 299	10.8	49.1	50	20	AA222993	5' primer used for	C 372	10.6	48.2	23	22	AA222993	Human chromosome 1
C 300	10.8	49.1	50	20	AA222993	5' primer used for	C 373	10.6	48.2	23	22	AA222993	Human chromosome 1
C 301	10.8	49.1	50	20	AA222993	5' primer used for	C 374	10.6	48.2	23	22	AA222993	Human chromosome 1

375	10.6	48.2	24	15	AA064954	Antisense oligonuc	C	448	10.6	48.2	36	21	AA061518	PCR primer used to
376	10.6	48.2	24	15	AA064954	Antisense oligonuc	C	449	10.6	48.2	36	21	AA062477	Barley D-hordein p
377	10.6	48.2	24	19	AA064954	Primer CYP2D6R us	C	450	10.6	48.2	36	21	AA062477	Barley D-hordein p
378	10.6	48.2	24	19	AA064954	Primer CYP2D6R us	C	451	10.6	48.2	36	21	AA062477	Hepatitis C virus
379	10.6	48.2	24	20	AA064954	Primer for ASTH1 p	C	452	10.6	48.2	36	21	AA029447	Hepatitis C virus
380	10.6	48.2	24	20	AA064954	Primer for ASTH1 p	C	453	10.6	48.2	37	20	AA029447	Pseudomonas sp. st
381	10.6	48.2	24	21	AA064954	Rat hepatocyte car	C	454	10.6	48.2	37	20	AA029447	Pseudomonas sp. st
382	10.6	48.2	24	21	AA064954	Rat hepatocyte car	C	455	10.6	48.2	37	20	AA029447	HCV detecting prim
383	10.6	48.2	24	21	AA064954	ASTH1 polymorphic	C	456	10.6	48.2	37	20	AA029447	HCV detecting prim
384	10.6	48.2	24	21	AA064954	ASTH1 polymorphic	C	457	10.6	48.2	37	22	AA027816	Human HFE gene w1
385	10.6	48.2	24	22	AA064954	Hepatitis C virus	C	458	10.6	48.2	37	22	AA027816	Human HFE gene w1
386	10.6	48.2	24	22	AA064954	Hepatitis C virus	C	459	10.6	48.2	37	22	AA027816	Human HFE gene w1
387	10.6	48.2	24	22	AA064954	Hepatitis C virus	C	460	10.6	48.2	37	22	AA027816	Human HFE gene w1
388	10.6	48.2	24	22	AA064954	aph(3')-Ia resista	C	461	10.6	48.2	38	16	AA090472	Human Kunitz-type
389	10.6	48.2	24	22	AA064954	aph(3')-Ia resista	C	462	10.6	48.2	38	16	AA090472	Human Kunitz-type
390	10.6	48.2	24	24	AB001236	Oligonucleotide ad	C	463	10.6	48.2	38	23	AB004312	Human NOGO Hammeth
391	10.6	48.2	24	24	AB001236	Oligonucleotide ad	C	464	10.6	48.2	38	23	AB004312	Human NOGO Hammeth
392	10.6	48.2	24	24	AB006397	Oligonucleotide ad	C	465	10.6	48.2	38	24	AB058497	Human CLCA1 gene e
393	10.6	48.2	24	24	AB006397	Oligonucleotide ad	C	466	10.6	48.2	38	24	AB058497	Human CLCA1 gene e
394	10.6	48.2	24	24	AB006438	Oligonucleotide ad	C	467	10.6	48.2	38	24	AB058497	Human ERG hammethe
395	10.6	48.2	24	24	AB006438	Oligonucleotide ad	C	468	10.6	48.2	38	24	AB058497	Human ERG hammethe
396	10.6	48.2	24	24	AB046270	Hepatitis C virus	C	469	10.6	48.2	38	24	AB019628	Human ERG hammethe
397	10.6	48.2	24	24	AB046270	Hepatitis C virus	C	470	10.6	48.2	38	24	AB019628	Human ERG hammethe
398	10.6	48.2	24	24	AB046270	Human CYP2D6 exon	C	471	10.6	48.2	39	20	AB019628	Human ERG hammethe
399	10.6	48.2	25	21	AA065551	Forward PCR primer	C	472	10.6	48.2	39	20	AA033234	PCR primer used to
400	10.6	48.2	25	21	AA065551	Forward PCR primer	C	473	10.6	48.2	40	12	AA013881	to HIV 18 subregion E
401	10.6	48.2	25	21	AA065551	Forward PCR primer	C	474	10.6	48.2	40	12	AA013881	HIV 18 subregion E
402	10.6	48.2	25	21	AA065551	Forward PCR primer	C	475	10.6	48.2	41	21	AA008115	Flavivirus nonstru
403	10.6	48.2	25	21	AA065551	HCV-specific ampli	C	476	10.6	48.2	41	21	AA008115	Flavivirus nonstru
404	10.6	48.2	25	21	AA065551	HCV-specific ampli	C	477	10.6	48.2	41	24	AA018049	Human polypeptide-
405	10.6	48.2	25	21	AA065551	Oligonucleotide SE	C	478	10.					

521	10.4	47.3	13	23	ABH56602	Oligonucleotide SE	C 594	10.4	47.3	24	24	ABQ03783	Oligonucleotide ad
C 522	10.4	47.3	13	23	ABH56602	Oligonucleotide SE	595	10.4	47.3	24	24	ABH84166	Capture oligonucle
C 523	10.4	47.3	13	23	ABH56603	Oligonucleotide SE	C 596	10.4	47.3	24	24	ABH84166	Capture oligonucle
C 524	10.4	47.3	13	23	ABH56603	Oligonucleotide SE	C 597	10.4	47.3	24	24	ABH84167	Capture oligonucle
C 525	10.4	47.3	14	20	AAA21642	Integrin alpha 6 s	C 598	10.4	47.3	24	24	ABH84167	Capture oligonucle
C 526	10.4	47.3	14	20	AAA21642	Integrin alpha 6 s	C 599	10.4	47.3	24	24	ABH84167	Capture oligonucle
C 527	10.4	47.3	16	21	AA61730	Primer for a gene	C 600	10.4	47.3	24	24	ABH84472	Capture oligonucle
C 528	10.4	47.3	16	21	AA61730	Primer for a gene	C 601	10.4	47.3	24	24	ABH84472	Capture oligonucle
C 529	10.4	47.3	16	22	AA506518	Mouse microglia an	C 602	10.4	47.3	24	24	ABH84473	Capture oligonucle
C 530	10.4	47.3	16	22	AA506518	Mouse microglia an	C 603	10.4	47.3	24	24	ABH84473	Capture oligonucle
C 531	10.4	47.3	17	20	AAA20792	Integrin alpha 6 s	C 604	10.4	47.3	24	24	ABH39370	Immunostimulatory
C 532	10.4	47.3	17	20	AAA20792	Integrin alpha 6 s	C 605	10.4	47.3	25	24	ABH39370	Immunostimulatory
C 533	10.4	47.3	17	20	AAA20793	Integrin alpha 6 s	C 606	10.4	47.3	25	24	ABH39370	Oligonucleotide ad
C 534	10.4	47.3	17	20	AAA20793	Integrin alpha 6 s	C 607	10.4	47.3	25	24	ABH39370	Oligonucleotide ad
C 535	10.4	47.3	18	22	AA796681	Human Akt-3 antis	C 608	10.4	47.3	26	16	AA796681	Bubble library. S
C 536	10.4	47.3	18	22	AA796681	Human Akt-3 antis	C 609	10.4	47.3	26	16	AA796681	Bubble library. S
C 537	10.4	47.3	20	16	AA085909	Primer SS20 for M1	C 610	10.4	47.3	26	24	ABH66804	Human gene specific
C 538	10.4	47.3	20	16	AA085909	Primer SS20 for M1	C 611	10.4	47.3	26	24	ABH66804	Human gene specific
C 539	10.4	47.3	20	16	AA085909	Primer SS20 for M1	C 612	10.4	47.3	27	22	AAH37939	SNP specific SNPE
C 540	10.4	47.3	20	18	AAV06723	M13mp2 Phage DNA P	C 613	10.4	47.3	27	22	AAH37939	SNP specific SNPE
C 541	10.4	47.3	20	19	AAV19469	Primer used to amp	C 614	10.4	47.3	28	22	AAH37717	SNP specific upper
C 542	10.4	47.3	20	19	AAV19469	Primer used to amp	C 615	10.4	47.3	28	22	AAH37717	SNP specific upper
C 543	10.4	47.3	20	21	AA681302	Mouse apoptosis-re	C 616	10.4	47.3	29	20	AAH19265	Integrin alpha 6 s
C 544	10.4	47.3	20	21	AA681302	Mouse apoptosis-re	C 617	10.4	47.3	29	20	AAH19265	Integrin alpha 6 s
C 545	10.4	47.3	20	21	AA681302	Hepatitis B virus	C 618	10.4	47.3	29	20	AAH19265	Mutagenic primer f
C 546	10.4	47.3	20	21	AA681302	Hepatitis B virus	C 619	10.4	47.3	29	20	AAH19265	Mutagenic primer f
C 547	10.4	47.3	20	21	AA681302	Hepatitis B virus	C 620	10.4	47.3	29	20	AAH19265	Human B-raf hamme
C 548	10.4	47.3	20	24	ABK92281	Human tumour suppr	C 621	10.4	47.3	29	21	AAH51002	Synthetic mutagen
C 549	10.4	47.3	20	24	ABK92281	Human tumour suppr	C 622	10.4	47.3	29	21	AAH51002	Synthetic mutagen
C 550	10.4	47.3	20	24	ABK92282	Human tumour suppr	C 623	10.4	47.3	29	24	AAH51002	A/ceal/HK/W312/97
C 551	10.4	47.3	20	24	ABK92282	Human tumour suppr	C 624	10.4	47.3	29	24	AAH51002	A/ceal/HK/W312/97
C 552	10.4	47.3	20	24	ABN80891	Human caspase 7 ph	C 625	10.4	47.3	30	21	AAZ49701	Duplex DNA-4 used
C 553	10.4	47.3	20	24	ABN80891	Human caspase 7 ph	C 626	10.4	47.3	30	21	AAZ49701	Duplex DNA-4 used
C 554	10.4	47.3	20	24	ABN80892	Human caspase 7 ph	C 627	10.4	47.3	31	15	AA065378	VH chain cDNA PCR
C 555	10.4	47.3	20	24	ABN80892	Human caspase 7 ph	C 628	10.4	47.3	31	15	AA065378	VH chain cDNA PCR
C 556	10.4	47.3	20	24	ABN80892	Capture oligonucle	C 629	10.4	47.3	31	15	AA065378	VH chain cDNA PCR
C 557	10.4	47.3	20	24	ABN80892	Capture oligonucle	C 630	10.4	47.3	31	15	AA065378	Hsp/2 PCR primer C
C 558	10.4	47.3	20	24	ABN80892	Capture oligonucle	C 631	10.4	47.3	31	15	AA065378	Hsp/2 PCR primer C
C 559	10.4	47.3	21	13	AAQ28662	ORH1 SENSE primer.	C 632	10.4	47.3	31	17	AA729014	Primer CG1FOR for
C 560	10.4	47.3	21	13	AAQ28662	ORH1 SENSE primer.	C 633	10.4	47.3	31	17	AA729014	Primer CG1FOR for
C 561	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 634	10.4	47.3	31	17	AA729014	Primer for mutine
C 562	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 635	10.4	47.3	31	18	AAV17274	Primer for mutine
C 563	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 636	10.4	47.3	31	18	AAV17274	Primer CG1FOR for
C 564	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 637	10.4	47.3	31	19	AAV56371	Primer CG1FOR for
C 565	10.4	47.3	21	20	AAZ20523	PCR primer for adh	C 638	10.4	47.3	31	19	AAV56371	Human ICAM-R cDNA
C 566	10.4	47.3	21	20	AAZ20523	PCR primer for adh	C 639	10.4	47.3	31	19	AAV56371	Human ICAM-R cDNA
C 567	10.4	47.3	21	20	AAZ20523	PCR primer for adh	C 640	10.4	47.3	31	19	AAV56371	Primer CG1FOR for
C 568	10.4	47.3	21	20	AAZ20523	PCR primer for adh	C 641	10.4	47.3	31	19	AAV56371	Primer CG1FOR for
C 569	10.4	47.3	21	20	AAZ20523	PCR primer for adh	C 642	10.4	47.3	31	19	AAV56371	Immunoglobulin V r
C 570	10.4	47.3	21	21	AA44878	Human uterine neck	C 643	10.4	47.3	31	19	AAV56371	Immunoglobulin V r
C 571	10.4	47.3	21	21	AA44878	Human uterine neck	C 644	10.4	47.3	31	20	AAV56371	Paragut binding a
C 572	10.4	47.3	21	21	AA44878	Human uterine neck	C 645	10.4	47.3	31	20	AAV56371	Paragut binding a
C 573	10.4	47.3	21	21	AA44878	Human uterine neck	C 646	10.4	47.3	31	20	AAV56371	Primer for antibod
C 574	10.4	47.3	21	24	AAK99082	S. aureus 16S H-7,	C 647	10.4	47.3	31	20	AAK21858	Primer for antibod
C 575	10.4	47.3	22	16	AA705569	Primer lacz 560 fo	C 648	10.4	47.3	31	20	AAK21858	Human biallelic po
C 576	10.4	47.3	22	16	AA705569	Primer lacz 560 fo	C 649	10.4	47.3	31	20	AAK21858	Human biallelic po
C 577	10.4	47.3	22	20	AAZ32481	ROSA beta-geo vect	C 650	10.4	47.3	31	20	AAK21858	Vh cDNA of ICR-8.1
C 578	10.4	47.3	22	20	AAZ32481	ROSA beta-geo vect	C 651	10.4	47.3	31	21	AAK21858	Vh cDNA of ICR-8.1
C 579	10.4	47.3	22	22	AAH44610	E. coli lacz RT-PC	C 652	10.4	47.3	31	21	AAK21858	Primer CG1FOR for
C 580	10.4	47.3	22	22	AAH44610	E. coli lacz RT-PC	C 653	10.4	47.3	31	21	AAK21858	Primer CG1FOR for
C 581	10.4	47.3	22	22	AAH44610	E. coli lacz RT-PC	C 654	10.4	47.3	31	21	AAK21858	Human genomic DNA
C 582	10.4	47.3	22	22	AAH44610	E. coli lacz RT-PC	C 655	10.4	47.3	31	21	AAK21858	Human genomic DNA
C 583	10.4	47.3	22	22	AAH44610	E. coli lacz RT-PC	C 656	10.4	47.3	31	21	AAK21858	Murine antibody IC
C 584	10.4	47.3	23	20	AAH88639	Human chromosome 1	C 657	10.4	47.3	31	21	AAK21858	Murine antibody IC
C 585	10.4	47.3	23	22	AAH88639	Human chromosome 1	C 658	10.4	47.3	31	21	AAK21858	Murine antibody IC
C 586	10.4	47.3	23	22	AAH88639	Human chromosome 1	C 659	10.4	47.3	31	21	AAK21858	Murine antibody IC
C 587	10.4	47.3	24	15	AAQ68528	Bacillus thuringie	C 660	10.4	47.3	31	22	AAQ68528	Murine A77 variabl
C 588	10.4	47.3	24	15	AAQ68528	Bacillus thuringie	C 661	10.4	47.3	31	22	AAQ68528	Murine A77 variabl
C 589	10.4	47.3	24	17	AA709123	cryIG gene primer	C 662	10.4	47.3	31	22	AAQ68528	Murine immunoglob
C 590	10.4	47.3	24	17	AA709123	cryIG gene primer	C 663	10.4	47.3	33	14	AAQ36445	Murine immunoglob
C 591	10.4	47.3	24	22	AA799632	Immunostimulatory	C 664	10.4	47.3	33	14	AAQ36445	Mutagenic primer C
C 592	10.4	47.3	24	22	AA799632	Immunostimulatory	C 665	10.4	47.3	33	18	AA787491	TRF T29 peptide se
C 593	10.4	47.3	24	24	ABQ03783	Oligonucleotide ad	C 666	10.4	47.3	33	18	AA787491	TRF T29 peptide se

667	10.4	47.3	33	20	AA35405	Probe for DNA enco	C 740	10.4	47.3	48	21	AA292895	Sindbis virus geno
C 668	10.4	47.3	33	20	AA35405	Probe for DNA enco	C 741	10.4	47.3	48	22	AA660417	FGF receptor 3 lig
C 669	10.4	47.3	33	22	AAH41200	PCR primer ADU001.	C 742	10.4	47.3	48	22	AA660417	FGF receptor 3 lig
C 670	10.4	47.3	33	22	AAH41200	PCR primer ADU001.	C 743	10.4	47.3	48	22	AA672714	Human PRO polypept
C 671	10.4	47.3	37	14	AAQ48279	Vibrio parahaeemoly	C 744	10.4	47.3	48	22	AA672714	Human PRO polypept
C 672	10.4	47.3	37	14	AAQ48279	Vibrio parahaeemoly	C 745	10.4	47.3	48	22	AA672714	Alphavirus related
C 673	10.4	47.3	38	24	AA167999	A/teal/HK/312/97	C 746	10.4	47.3	48	24	AA138775	Alphavirus related
C 674	10.4	47.3	38	24	AA167999	A/teal/HK/312/97	C 747	10.4	47.3	48	24	ABK46241	Sindbis virus geno
C 675	10.4	47.3	39	17	AA140080	Primer for bcl-XS	C 748	10.4	47.3	48	24	ABK46241	Sindbis virus geno
C 676	10.4	47.3	39	17	AA140080	Primer for bcl-XS	C 749	10.4	47.3	48	24	AAH99927	Sindbis virus geno
C 677	10.4	47.3	39	21	AA427123	Chlamydia pneumoni	C 750	10.4	47.3	48	24	AAH99927	Primer 2 used to a
C 678	10.4	47.3	39	21	AA427123	Chlamydia pneumoni	C 751	10.4	47.3	48	24	AAH99927	Primer 2 used to a
C 679	10.4	47.3	39	21	AA427123	Chlamydia pneumoni	C 752	10.4	47.3	48	24	ABK03387	Sindbis virus non
C 680	10.4	47.3	40	15	AA050313	Detection probe 5.	C 753	10.4	47.3	49	21	AA03387	Sindbis virus non
C 681	10.4	47.3	40	15	AA050313	Detection probe 5.	C 754	10.4	47.3	49	21	AA03387	Detection of nucle
C 682	10.4	47.3	40	15	AA050313	Detection probe 5.	C 755	10.4	47.3	49	21	AA03387	Detection of nucle
C 683	10.4	47.3	40	15	AA050313	Detection probe 5.	C 756	10.4	47.3	50	18	AAV77788	Staphylococcus aur
C 684	10.4	47.3	40	15	AA050313	Detection probe 5.	C 757	10.4	47.3	50	18	AAV77788	Staphylococcus aur
C 685	10.4	47.3	40	15	AA050313	Detection probe 5.	C 758	10.4	47.3	50	21	AAV77788	Staphylococcus aur
C 686	10.4	47.3	40	18	AA147465	Foldback triplex f	C 759	10.4	47.3	50	21	AAV77788	Human bone marrow
C 687	10.4	47.3	40	21	AA295865	Poly nucleotide seq	C 760	10.4	47.3	50	22	AA130444	Human bone marrow
C 688	10.4	47.3	40	21	AA295865	Poly nucleotide seq	C 761	10.4	47.3	50	22	AA130444	Human bone marrow
C 689	10.4	47.3	40	21	AA295865	Poly nucleotide seq	C 762	10.4	47.3	50	22	AA130444	Human bone marrow
C 690	10.4	47.3	40	24	ABN88576	Isoprenoid related	C 763	10.2	46.4	14	14	AA043637	Human SNP oligonc
C 691	10.4	47.3	40	24	ABN88576	Isoprenoid related	C 764	10.2	46.4	14	14	AA043637	Human SNP oligonc
C 692	10.4	47.3	40	24	ABN88576	Isoprenoid related	C 765	10.2	46.4	17	19	AAV95838	Human SNP oligonc
C 693	10.4	47.3	40	24	ABN88576	Isoprenoid related	C 766	10.2	46.4	17	19	AAV95838	Human SNP oligonc
C 694	10.4	47.3	40	24	ABN88576	Isoprenoid related	C 767	10.2	46.4	17	21	AA36226	Human SNP oligonc
C 695	10.4	47.3	41	13	AAQ31831	Coagulation factor	C 768	10.2	46.4	17	21	AA36226	Human SNP oligonc
C 696	10.4	47.3	41	13	AAQ31831	Coagulation factor	C 769	10.2	46.4	17	21	AA36226	Human SNP oligonc
C 697	10.4	47.3	41	13	AAQ31831	Coagulation factor	C 770	10.2	46.4	17	21	AA36226	Human SNP oligonc
C 698	10.4	47.3	41	13	AAQ31831	Coagulation factor	C 771	10.2	46.4	18	24	AB135558	Human genomic SNP
C 699	10.4	47.3	41	13	AAQ31831	Coagulation factor	C 772	10.2	46.4	18	24	AB135558	Human genomic SNP
C 700	10.4	47.3	43	18	AA147467	Probe GGP105-145.	C 773	10.2	46.4	20	14	AA048563	Immunostimulatory
C 701	10.4	47.3	43	18	AA147467	Probe GGP105-145.	C 774	10.2	46.4	20	14	AA048563	Immunostimulatory
C 702	10.4	47.3	43	22	AA689694	Foldback triplex f	C 775	10.2	46.4	20	15	AA065418	HPV E6/7 region pr
C 703	10.4	47.3	43	22	AA689694	Foldback triplex f	C 776	10.2	46.4	20	15	AA065418	HPV E6/7 region pr
C 704	10.4	47.3	47	14	AAQ47803	Probe used to iden	C 777	10.2	46.4	20	17	AA116094	Primer to amplify
C 705	10.4	47.3	47	14	AAQ47803	Probe used to iden	C 778	10.2	46.4	20	17	AA116094	Primer to amplify
C 706	10.4	47.3	47	20	AAV72468	Bilirubin oxidase	C 779	10.2	46.4	20	17	AA116094	Nia PCR primer NSX
C 707	10.4	47.3	47	20	AAV72468	Bilirubin oxidase	C 780	10.2	46.4	20	20	AA206117	PCR primer used to
C 708	10.4	47.3	47	21	AA266475	Human PRO533 clone	C 781	10.2	46.4	20	20	AA206117	PCR primer used to
C 709	10.4	47.3	47	21	AA266475	Human PRO533 clone	C 782	10.2	46.4	20	20	AA206117	PCR primer used to
C 710	10.4	47.3	47	21	AA266475	Human PRO533 clone	C 783	10.2	46.4	20	20	AA206117	PCR primer used to
C 711	10.4	47.3	47	21	AA266475	Human PRO533 clone	C 784	10.2	46.4	20	20	AA206117	PCR primer used to
C 712	10.4	47.3	48	16	AA086156	Human map-related	C 785	10.2	46.4	20	20	AA206117	PCR primer used to
C 713	10.4	47.3	48	16	AA086156	Human map-related	C 786	10.2	46.4	20	20	AA206117	PCR primer used to
C 714	10.4	47.3	48	17	AA135055	Sindbis virus geno	C 787	10.2	46.4	20	22	AA660154	Human ATM gene exo
C 715	10.4	47.3	48	17	AA135055	Sindbis virus geno	C 788	10.2	46.4	20	22	AA660154	Human ATM gene exo
C 716	10.4	47.3	48	17	AA135055	Sindbis virus geno	C 789	10.2	46.4	20	24	ABK70814	Human TSP1 domain
C 717	10.4	47.3	48	18	AA135055	Sindbis virus geno	C 790	10.2	46.4	20	24	ABK70814	Human TSP1 domain
C 718	10.4	47.3	48	18	AA135055	Sindbis virus geno	C 791	10.2	46.4	20	24	ABK70814	Human TSP1 domain
C 719	10.4	47.3	48	19	AAV60128	Primer SP6-1A used	C 792	10.2	46.4	20	24	ABK70814	PCR primer used to
C 720	10.4	47.3	48	19	AAV60128	Primer SP6-1A used	C 793	10.2	46.4	20	24	ABK70814	PCR primer used to
C 721	10.4	47.3	48	19	AAV60128	Primer SP6-1A used	C 794	10.2	46.4	20	24	ABK70814	PCR primer used to
C 722	10.4	47.3	48	19	AAV60128	Primer SP6-1A used	C 795	10.2	46.4	20	24	ABK70814	PCR primer used to
C 723	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 796	10.2	46.4	20	24	ABK70814	PCR primer used to
C 724	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 797	10.2	46.4	20	24	ABK70814	PCR primer used to
C 725	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 798	10.2	46.4	21	13	AA032568	HPV E6/7 region pr
C 726	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 799	10.2	46.4	21	13	AA032568	HPV E6/7 region pr
C 727	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 800	10.2	46.4	21	14	AA048540	HPV E6/7 region pr
C 728	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 801	10.2	46.4	21	14	AA048540	HPV E6/7 region pr
C 729	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 802	10.2	46.4	21	14	AA048540	HPV E6/7 region pr
C 730	10.4	47.3	48	20	AAV42367	Primer SP6-1A used	C 803	10.2	46.4	21	14	AA048540	HPV E6/7 region pr
C 731	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 804	10.2	46.4	21	19	AA225833	Human polymorphic
C 732	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 805	10.2	46.4	21	19	AA225833	Human polymorphic
C 733	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 806	10.2	46.4	21	19	AA225833	Human polymorphic
C 734	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 807	10.2	46.4	21	19	AA225833	Human polymorphic
C 735	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 808	10.2	46.4	21	24	ABK83411	Polymerase express
C 736	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 809	10.2	46.4	21	24	ABK83411	Polymerase express
C 737	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 810	10.2	46.4	21	24	ABK83411	Polymerase express
C 738	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 811	10.2	46.4	22	21	AA68654	NT3-Fab antibody f
C 739	10.4	47.3	48	21	AAV70687	Primer for bcl-XS	C 812	10.2	46.4	22	21	AA68654	NT3-Fab antibody f

C 813	10.2	46.4	22	22	AAF98756	Human IFN-alpha im	C 886	10.2	46.4	30	15	AAQ70653	PCR primer BAMLINK
C 814	10.2	46.4	22	22	AAF98756	Human IFN-alpha im	C 887	10.2	46.4	30	17	AAI38777	SRV-1 primer 1 for
C 815	10.2	46.4	22	22	AAF99770	Immunostimulatory	C 888	10.2	46.4	30	17	AAI38777	SRV-1 primer 1 for
C 816	10.2	46.4	22	22	AAF99770	Immunostimulatory	C 889	10.2	46.4	30	20	AAV99980	Nucleotide sequenc
C 817	10.2	46.4	22	22	AAF99839	Immunostimulatory	C 890	10.2	46.4	30	20	AAV99980	Nucleotide sequenc
C 818	10.2	46.4	22	22	AAF99839	Immunostimulatory	C 891	10.2	46.4	30	22	AAA91591	PCR primer for S.
C 819	10.2	46.4	23	19	AAQ09982	Human biallelic po	C 892	10.2	46.4	30	22	AAA91591	PCR primer for S.
C 820	10.2	46.4	23	19	AAQ09982	Human biallelic po	C 893	10.2	46.4	30	22	AAA37872	Temamyl-1-like alph
C 821	10.2	46.4	23	19	AAV61032	Plant embryo-speci	C 894	10.2	46.4	30	22	AAA37872	Temamyl-1-like alph
C 822	10.2	46.4	23	19	AAV61032	Plant embryo-speci	C 895	10.2	46.4	30	24	ABK70816	Human TSPI domain
C 823	10.2	46.4	23	20	AAK84529	PCR primer for p90	C 896	10.2	46.4	30	24	ABK70816	Human TSPI domain
C 824	10.2	46.4	23	20	AAK84529	PCR primer for p90	C 897	10.2	46.4	31	22	AAI29920	Human single nucle
C 825	10.2	46.4	23	21	AAZ45845	PCR primer used am	C 898	10.2	46.4	31	22	AAI29920	Human single nucle
C 826	10.2	46.4	23	21	AAZ45845	PCR primer used am	C 899	10.2	46.4	31	22	AAI30199	Human single nucle
C 827	10.2	46.4	23	22	AAI16921	PCR primer #3, use	C 900	10.2	46.4	31	22	AAI30199	Human single nucle
C 828	10.2	46.4	23	22	AAI16921	PCR primer #3, use	C 901	10.2	46.4	32	21	AAA63981	PCR primer used to
C 829	10.2	46.4	24	10	AAAN91579	Probe 1 for the de	C 902	10.2	46.4	32	21	AAA63981	PCR primer used to
C 830	10.2	46.4	24	10	AAAN91579	Probe 1 for the de	C 903	10.2	46.4	32	21	AAZ49811	Primer Alex2 used
C 831	10.2	46.4	24	10	AAAN93011	Probe for detectin	C 904	10.2	46.4	32	21	AAZ49811	Primer Alex2 used
C 832	10.2	46.4	24	10	AAAN93011	Probe for detectin	C 905	10.2	46.4	33	13	AAQ31153	Probe 122 for geno
C 833	10.2	46.4	24	16	AAQ76194	Degenerate "nested	C 906	10.2	46.4	33	13	AAQ31153	Probe 122 for geno
C 834	10.2	46.4	24	16	AAQ76194	Degenerate "nested	C 907	10.2	46.4	33	14	AAQ46459	Hepatitis C virus
C 835	10.2	46.4	24	20	AAK33754	DNA tandem nucleot	C 908	10.2	46.4	33	14	AAQ46459	Hepatitis C virus
C 836	10.2	46.4	24	20	AAK33754	DNA tandem nucleot	C 909	10.2	46.4	33	19	AAV07856	HCV.33.4 capture p
C 837	10.2	46.4	24	20	AAK33721	DNA tandem nucleot	C 910	10.2	46.4	33	19	AAV07856	HCV.33.4 capture p
C 838	10.2	46.4	24	20	AAK33721	DNA tandem nucleot	C 911	10.2	46.4	33	20	AAV83084	Capture probe HCV.
C 839	10.2	46.4	24	24	ABO91872	M. capsulatus ORF	C 912	10.2	46.4	33	20	AAV83084	Capture probe HCV.
C 840	10.2	46.4	24	24	ABO91872	M. capsulatus ORF	C 913	10.2	46.4	33	24	ABA04379	AtRRF3 PCR primer
C 841	10.2	46.4	24	24	ABI83394	Capture oligonucle	C 914	10.2	46.4	33	24	ABA04379	AtRRF3 PCR primer
C 842	10.2	46.4	24	24	ABI83394	Capture oligonucle	C 915	10.2	46.4	33	24	AAV38418	Primer K31C1 for p
C 843	10.2	46.4	24	24	ABI83395	Capture oligonucle	C 916	10.2	46.4	34	19	AAV38418	Primer K31C1 for p
C 844	10.2	46.4	24	24	ABI83395	Capture oligonucle	C 917	10.2	46.4	34	19	AAV38418	Primer K31C1 for p
C 845	10.2	46.4	24	24	ABI84502	Capture oligonucle	C 918	10.2	46.4	35	19	AAV45317	FvK forward primer
C 846	10.2	46.4	24	24	ABI84502	Capture oligonucle	C 919	10.2	46.4	35	19	AAV45317	FvK forward primer
C 847	10.2	46.4	24	24	ABI84503	Capture oligonucle	C 920	10.2	46.4	36	14	AAQ48270	Vibrio alginolytic
C 848	10.2	46.4	24	24	ABI84503	Capture oligonucle	C 921	10.2	46.4	36	16	AAI5418	Human re1a hamme
C 849	10.2	46.4	24	24	ABI84542	Capture oligonucle	C 922	10.2	46.4	36	16	AAI5418	Human re1a hamme
C 850	10.2	46.4	24	24	ABI84642	Capture oligonucle	C 923	10.2	46.4	36	16	AAI57532	RSV N hammerhead r
C 851	10.2	46.4	24	24	ABI84643	Capture oligonucle	C 924	10.2	46.4	36	16	AAI57532	RSV N hammerhead r
C 852	10.2	46.4	24	24	ABI84643	Capture oligonucle	C 925	10.2	46.4	36	16	AAI575180	RSV IC hammerhead
C 853	10.2	46.4	24	24	ABI87530	Capture oligonucle	C 926	10.2	46.4	36	16	AAI57180	RSV IC hammerhead
C 854	10.2	46.4	24	24	ABI87530	Capture oligonucle	C 927	10.2	46.4	36	16	AAI49962	Human CERP HH ribo
C 855	10.2	46.4	24	24	ABI87531	Capture oligonucle	C 928	10.2	46.4	36	17	AAI49962	Human CERP HH ribo
C 856	10.2	46.4	24	24	ABI87531	Capture oligonucle	C 929	10.2	46.4	36	17	AAI49969	Human CERP HH ribo
C 857	10.2	46.4	24	24	ABI90956	Capture oligonucle	C 930	10.2	46.4	36	17	AAI49969	Human CERP HH ribo
C 858	10.2	46.4	24	24	ABI90956	Capture oligonucle	C 931	10.2	46.4	36	21	AAZ43136	PCR primer for C.
C 859	10.2	46.4	24	24	ABI90957	Capture oligonucle	C 932	10.2	46.4	36	21	AAZ43136	PCR primer for C.
C 860	10.2	46.4	24	24	ABI90957	Capture oligonucle	C 933	10.2	46.4	37	21	AAI72807	Human insulin-like
C 861	10.2	46.4	24	24	ABI91662	Capture oligonucle	C 934	10.2	46.4	37	21	AAI72807	Human insulin-like
C 862	10.2	46.4	24	24	ABI91662	Capture oligonucle	C 935	10.2	46.4	37	21	AAI72910	Human insulin-like
C 863	10.2	46.4	24	24	ABI91663	Capture oligonucle	C 936	10.2	46.4	37	21	AAI72910	Human insulin-like
C 864	10.2	46.4	24	24	ABI91663	Capture oligonucle	C 937	10.2	46.4	37	22	AAH49869	Bacterial 23S/5S R
C 865	10.2	46.4	26	24	ABK71095	Mouse HYPLIP1 locu	C 938	10.2	46.4	37	22	AAH49869	Bacterial 23S/5S R
C 866	10.2	46.4	26	24	ABK71095	Mouse HYPLIP1 locu	C 939	10.2	46.4	37	24	ABK94544	Human MHC class I
C 867	10.2	46.4	26	24	ABK68191	Mouse HYPLIP1 locu	C 940	10.2	46.4	37	24	ABK94544	Human MHC class I
C 868	10.2	46.4	26	24	ABK68191	Mouse HYPLIP1 locu	C 941	10.2	46.4	37	24	ABA95558	Human IGF-1 PCR pr
C 869	10.2	46.4	27	18	AAFG6353	Variable light cha	C 942	10.2	46.4	37	24	ABA95558	Human IGF-1 PCR pr
C 870	10.2	46.4	27	18	AAFG6353	Variable light cha	C 943	10.2	46.4	38	15	AAQ73036	Tyrosine-kinase sy
C 871	10.2	46.4	28	13	AAQ32727	Mouse light chain	C 944	10.2	46.4	38	15	AAQ73036	Tyrosine-kinase sy
C 872	10.2	46.4	28	13	AAQ32727	Mouse light chain	C 945	10.2	46.4	38	15	AAQ73037	Tyrosine-kinase sy
C 873	10.2	46.4	28	22	AAF82008	1.0 kb DNA fragmen	C 946	10.2	46.4	38	15	AAQ73037	Tyrosine-kinase sy
C 874	10.2	46.4	28	22	AAF82008	1.0 kb DNA fragmen	C 947	10.2	46.4	38	18	AAI51264	Human AD4 gene gen
C 875	10.2	46.4	28	22	AAF82008	1.0 kb DNA fragmen	C 948	10.2	46.4	38	18	AAI51264	Human AD4 gene gen
C 876	10.2	46.4	28	22	AAF82008	1.0 kb DNA fragmen	C 949	10.2	46.4	38	22	AAH42703	PCR primer used to
C 877	10.2	46.4	28	24	ABU55961	Mouse light chain	C 950	10.2	46.4	38	22	AAH42703	PCR primer used to
C 878	10.2	46.4	28	24	ABU55961	Mouse light chain	C 951	10.2	46.4	38	22	AAH37871	Temamyl-1-like alph
C 879	10.2	46.4	29	19	AAV46267	Human corticostatin	C 952	10.2	46.4	38	22	AAH37871	Temamyl-1-like alph
C 880	10.2	46.4	29	19	AAV46267	Human corticostatin	C 953	10.2	46.4	38	22	AAK04311	Human NOGO Hamme
C 881	10.2	46.4	29	21	AAA04380	Polymorphic fragme	C 954	10.2	46.4	38	23	AAK04311	Human NOGO Hamme
C 882	10.2	46.4	29	21	AAA04380	Polymorphic fragme	C 955	10.2	46.4	38	24	ABK57867	Human CLCA1 gene e
C 883	10.2	46.4	30	10	AAAN91936	Variable portion o	C 956	10.2	46.4	38	24	ABK57867	Human CLCA1 gene e
C 884	10.2	46.4	30	10	AAAN91936	Variable portion o	C 957	10.2	46.4	38	24	ABK58916	Human CLCA1 gene e
C 885	10.2	46.4	30	15	AAQ70653	PCR primer BAMLINK	C 958	10.2	46.4	38	24	ABK58916	Human CLCA1 gene e

PN .MO9845468-A1.
XX
PD 15-OCT-1998.
XX
PF 07-APR-1998; 98WO-US06826.
XX
PR 08-APR-1997; 97US-0043205.
XX
PA (USAS) NASA US NAT AERO & SPACE ADMIN.
PA (TULA) TULANE EDUCATIONAL FUND.
XX
PI Goodwin TJ, Hammond TG, Kaysen JH;
XX
DR WPI; 1998-594488/50.
XX
PT Production of functional proteins - by culturing cells under
PT microgravity conditions, and inducing gene expression with
PT oligonucleotide directed against shear stress response element
XX
PS Example 16; Fig 4A; 55pp; English.
XX
CC The present sequence represents an antisense probe for the shear
CC response element. The probe has two possible conformations. As a singular
CC strand it can fold back on itself to form a binding element for the
CC transcription factor. As a double strand, it has two binding sites for
CC the transcription factor (both in the sense and antisense orientation).
CC The specification describes the expression of at least 1 gene which
CC is induced in a cell by treating with a transcription factor decoy
CC oligonucleotide directed against a sequence encoding a shear stress
CC response element (SSRE). The method is used to produce hormones, toxin
CC receptors and shear stress-dependent molecules, e.g. erythropoietin
CC (EPO) for treatment of anaemia in dialysis or AIDS patients, and many
CC forms of cancer. Also cells expressing these molecules are useful for
CC biochemical, toxicological or pharmacological studies or as hormone
CC implants.
XX
SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 other;
XX
Query Match 100.0%; Score 22; DB 19; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGTCTCAG 22
Db 22 CTGAGACCGATATCGGTCTCAG 1
XX
RESULT 3
AAA70834
ID AAA70834 standard; RNA; 28 BP.
XX
AC AAA70834;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #34.
XX
KM Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Mus sp.
XX
PN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US10361.
XX
PR 12-MAY-1998; 98US-0076404.
PR 12-MAY-1998; 98US-0085092.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;

PI Hofstadler S, McNeil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds -
XX
PS Claim 275; Page 238; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses
CC 3-dimensional representations of the biomolecule and a library of
CC compounds and comprises (a) identifying at least one molecular
CC interaction site of the target RNA; (b) generating in silico a virtual
CC library of compounds predicted or calculated to interact with the
CC molecular interaction site; and (c) comparing 3-dimensional (3-D)
CC representations of the target RNA with members of the virtual library of
CC compounds to generate a hierarchy of the compounds ranked in accordance
CC with their respective ability to form physical interactions with the
CC molecular interaction site. The method also describes (1) RNA comprising
CC a joined sequence of at least 24 nucleotides but not more than 70
CC nucleotides and having secondary structure defined by: (a) 3 nucleotides
CC forming a first side of a first double stranded (ds) region; (b) 2
CC nucleotides forming a first side of an internal loop region; (c) 4
CC nucleotides forming a first side of a second ds region; (d) 4 or 5
CC nucleotides forming an end loop region; (e) 4 nucleotides forming a
CC second side of the second ds region; (f) 4 nucleotides forming a second
CC side of the internal loop region; and (g) 3 nucleotides forming a second
CC side of the first ds region; (2) a purified and isolated RNA fragment
CC comprising the human sequence UUUACACUAUUCUGUACAGAAAUUC (11). The
CC methods and products can be used for identifying agents which modulate
CC the activity of biomolecules, particularly RNA. Such agents can be used
CC as pharmaceutical, agricultural or industrial compounds.
XX
SQ Sequence 28 BP; 11 A; 8 C; 4 G; 5 U; 0 other;
XX
Query Match 64.5%; Score 14.2; DB 21; Length 28;
Best Local Similarity 68.4%; Pred. No.: 9.2e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 GAGACCGATATCGGTCTCA 21
Db 1 GAGACCCAAUUCUGUCUA 19
XX
RESULT 4
AAA70834/c
ID AAA70834 standard; RNA; 28 BP.
XX
AC AAA70834;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #34.
XX
KM Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Mus sp.
XX
PN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US10361.
XX
PR 12-MAY-1998; 98US-0076404.
PR 12-MAY-1998; 98US-0085092.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, McNeil J;

XX WPI; 2000-086439/07.
DR Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds -
XX
PS Claim 275; Page 238; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses
CC 3-dimensional representations of the biomolecule and a library of
CC compounds and comprises (a) identifying at least one molecular
CC interaction site of the target RNA; (b) generating in silico a virtual
CC library of compounds predicted or calculated to interact with the
CC molecular interaction site; and (c) comparing 3-dimensional (3-D)
CC representations of the target RNA with members of the virtual library of
CC compounds to generate a hierarchy of the compounds ranked in accordance
CC with their respective ability to form physical interactions with the
CC molecular interaction site. The method also describes (1) RNA comprising
CC a joined sequence of at least 24 nucleotides but not more than 70
CC nucleotides and having secondary structure defined by: (a) 3 nucleotides
CC forming a first side of a first double stranded (ds) region; (b) 2
CC nucleotides forming a first side of an internal loop region; (c) 4
CC nucleotides forming a first side of a second ds region; (d) 4 or 5
CC nucleotides forming an end loop region; (e) 4 nucleotides forming a
CC second side of the second ds region; (f) 4 nucleotides forming a
CC side of the internal loop region; and (g) 3 nucleotides forming a second
CC side of the first ds region; (2) a purified and isolated RNA fragment
CC comprising the human sequence UUUACACUAAUUCUGUUGUACGAAAUUC (11). The
CC methods and products can be used for identifying agents which modulate
CC the activity of biomolecules, particularly RNA. Such agents can be used
CC as pharmaceutical, agricultural or industrial compounds.
SQ Sequence 28 BP; 11 A; 8 C; 4 G; 5 U; 0 other;
XX
SQ
Query Match 64.5%; Score 14.2; DB 21; Length 28;
Best Local Similarity 84.2%; Pred. No. 9.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGGTCTC 20
DB 19 TGAGACGAGATTGGGTCTC 1
RESULT 5
ABA98894
ID ABA98894 standard; DNA; 33 BP.
XX
AC ABA98894;
XX
DT 07-MAY-2002 (first entry)
XX
DE DNA sequence 2 relative to the farnesyltransferase of the invention.
XX
KM Farnesyltransferase; enzyme; ds.
XX
OS Unidentified.
XX
PN KR98075770-A.
XX
PD 16-NOV-1998.
XX
PF 01-APR-1997; 97KR-0012067.
XX
PR 01-APR-1997; 97KR-0012067.
XX
PA (GLDS) LG CHEM LTD.
XX
PI Moon GD, Kim MJ, Chung HH;
XX
DR WPI; 2000-020309/02.
XX

PT Farnesyltransferase having histidine tag and process for preparing the
PT same.
XX
PS Disclosure; Page 9; 23pp; Korean.
XX
CC The invention relates to a farnesyltransferase with a histidine tag,
CC and methods for preparing it. The current sequence represents DNA
CC sequence 2 relative to the farnesyltransferase of the invention.
XX
SQ Sequence 33 BP; 8 A; 8 C; 12 G; 5 T; 0 other;
XX
SQ
Query Match 63.6%; Score 14; DB 21; Length 33;
Best Local Similarity 77.3%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGTCTCAG 22
DB 2 CCGGATCGATATCGGTACAG 23
RESULT 6
ABA98894/C
ID ABA98894 standard; DNA; 33 BP.
XX
AC ABA98894;
XX
DT 07-MAY-2002 (first entry)
XX
DE DNA sequence 2 relative to the farnesyltransferase of the invention.
XX
KM Farnesyltransferase; enzyme; ds.
XX
OS Unidentified.
XX
PN KR98075770-A.
XX
PD 16-NOV-1998.
XX
PF 01-APR-1997; 97KR-0012067.
XX
PR 01-APR-1997; 97KR-0012067.
XX
PA (GLDS) LG CHEM LTD.
XX
PI Moon GD, Kim MJ, Chung HH;
XX
DR WPI; 2000-020309/02.
XX
PT Farnesyltransferase having histidine tag and process for preparing the
PT same.
XX
PS Disclosure; Page 9; 23pp; Korean.
XX
CC The invention relates to a farnesyltransferase with a histidine tag,
CC and methods for preparing it. The current sequence represents DNA
CC sequence 2 relative to the farnesyltransferase of the invention.
XX
SQ Sequence 33 BP; 8 A; 8 C; 12 G; 5 T; 0 other;
XX
SQ
Query Match 63.6%; Score 14; DB 21; Length 33;
Best Local Similarity 77.3%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGTCTCAG 22
DB 23 CTGCTACGATATCGATCCCG 2
RESULT 7
AA295872
ID AA295872 standard; DNA; 40 BP.
XX
AC AA295872;
XX


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XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX WPI; 2001-418294/44.
XX
PT Hexapetaloid duplicon containing transferase 11 and encoded
PT polynucleotide, applicable in diagnosis and treatment of malignant
PT tumor, hemopathy, HIV infection, immunological diseases and various
PT inflammation -
XX
PS Example 5; Page 18; 35pp; Chinese.
XX
CC The invention relates to human hexapetaloid duplicon-containing
CC transferase 11 (AA897610), nucleic acids encoding it (AA46197), and a
CC method for the recombinant production of hexapetaloid duplicon-containing
CC transferase 11. The present invention additionally discloses an
CC antagonist of hexapetaloid duplicon-containing transferase 11 for
CC therapeutic use, and an antibody which specifically binds to the protein.
CC Hexapetaloid duplicon-containing transferase 11, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders and inflammatory conditions. The protein may
CC also be used to screen for modulators of its activity or for peptide
CC fingerprinting identification. The polynucleotide can be used as a primer
CC for nucleic acid amplification reactions or as a probe for hybridisation
CC reactions, or in producing gene chips or microarrays. Sequences
CC AA46200-AA46201 represent PCR primers used in an exemplification of
CC the invention to amplify human hexapetaloid duplicon-containing
CC transferase 11 cDNA for cloning.
XX
SQ Sequence 33 BP; 9 A; 8 C; 9 G; 7 T; 0 other;
XX
Query Match 61.8%; Score 13.6; DB 22; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 3 GAGACGATATCGCTCAG 22
DB 14 GAGATCGATCATCTGAG 33
XX
RESULT 10
AA46201/c
ID AA46201 standard; DNA; 33 BP.
XX
AC AA46201;
XX
DT 21-SEP-2001 (first entry)
XX
DE Hexapetaloid duplicon-containing transferase 11 PCR primer, SEQ ID NO:6.
XX
KW Hexapetaloid duplicon-containing transferase 11; human;
KW recombinant production; malignant tumour; cancer; blood disease;
KW HIV infection; human immunodeficiency virus; immune disorder;
KW inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
KW immunomodulator; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200148222-A1.
XX
XX PD 05-JUL-2001.
XX
XX PF 25-DEC-2000; 2000WO-CN00719.
XX
XX PR 27-DEC-1999; 99CN-0125376.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
```

```
DR WPI; 2001-418294/44.
XX
XX Hexapetaloid duplicon containing transferase 11 and encoded
XX PT polynucleotide, applicable in diagnosis and treatment of malignant
XX PT tumor, hemopathy, HIV infection, immunological diseases and various
XX PT inflammation -
XX
XX PS Example 5; Page 18; 35pp; Chinese.
XX
CC The invention relates to human hexapetaloid duplicon-containing
CC transferase 11 (AA897610), nucleic acids encoding it (AA46197), and a
CC method for the recombinant production of hexapetaloid duplicon-containing
CC transferase 11. The present invention additionally discloses an
CC antagonist of hexapetaloid duplicon-containing transferase 11 for
CC therapeutic use, and an antibody which specifically binds to the protein.
CC Hexapetaloid duplicon-containing transferase 11, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders and inflammatory conditions. The protein may
CC also be used to screen for modulators of its activity or for peptide
CC fingerprinting identification. The polynucleotide can be used as a primer
CC for nucleic acid amplification reactions or as a probe for hybridisation
CC reactions, or in producing gene chips or microarrays. Sequences
CC AA46200-AA46201 represent PCR primers used in an exemplification of
CC the invention to amplify human hexapetaloid duplicon-containing
CC transferase 11 cDNA for cloning.
XX
SQ Sequence 33 BP; 9 A; 8 C; 9 G; 7 T; 0 other;
XX
Query Match 61.8%; Score 13.6; DB 22; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 CTGAGACGATATCGCTC 20
DB 33 CTCGACTGATCTGATCTC 14
XX
RESULT 11
AB195602
ID AB195602 standard; DNA; 20 BP.
XX
AC AB195602;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
XX Synthetic.
XX
XX WO200179548-A2.
XX
XX PD 25-OCT-2001.
XX
XX PF 04-APR-2001; 2001WO-US10958.
XX
XX PR 14-APR-2000; 2000US-197271P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zivri M, Gerry NP, Favis R, Kliman R;
XX
XX WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX PT complementary oligonucleotides hybridize with little mismatch -
XX
```


PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. *Salmonella*, *Listeria monocytogenes* and *Haemophilus influenza*, fungal
CC infectious agents e.g. *Cryptococcus neoformans*, *Candida albicans* and
CC *Aspergillus fumigatus*, viruses e.g. T-cell lymphocytotropic citus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from *Onchocerca volvulus*, *Entamoeba histolytica* and *Dracunculus*
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 other;
XX
Query Match 60.9%; Score 13.4; DB 24; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 8 CGATATCGGTCTGAC 22
| | | | | | | | | | | | | | | | | | | | | |
Db 5 CCAATCGGTCTGAC 19
XX
RESULT 12
AB195602/c
ID AB195602 standard; DNA; 20 BP.
XX
AC AB195602;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. *Salmonella*, *Listeria monocytogenes* and *Haemophilus influenza*, fungal
CC infectious agents e.g. *Cryptococcus neoformans*, *Candida albicans* and
CC *Aspergillus fumigatus*, viruses e.g. T-cell lymphocytotropic citus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from *Onchocerca volvulus*, *Entamoeba histolytica* and *Dracunculus*
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 other;
XX
Query Match 60.9%; Score 13.4; DB 24; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 CTGAGACCGATATCG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 19 CTGAGACCGATATCG 5
XX
RESULT 13
AB187774
ID AB187774 standard; DNA; 24 BP.
XX
AC AB187774;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 25; 300bp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SO Sequence 24 BP; 3 A; 8 C; 6 G; 7 T; 0 other;
Query Match 60.9%; Score 13.4; DB 24; Length 24;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 8 CGATATCGGTCTCAG 22
DB 5 CCAATGCGTCTCAG 19
RESULT 14
AB187774/c
ID AB187774 standard; DNA; 24 BP.
XX
AC AB187774;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #1.
XX
KW Human; K-raas; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
WI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 25; 300bp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SO Sequence 24 BP; 3 A; 8 C; 6 G; 7 T; 0 other;
Query Match 60.9%; Score 13.4; DB 24; Length 24;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CTGAGACCGATATCG 15
DB 19 CTGAGACCGATATCG 5
RESULT 15
AB187775
ID AB187775 standard; DNA; 24 BP.
XX
AC AB187775;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #2.
XX
KW Human; K-raas; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
WI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -

P8 Example 5; Fig 25; 300bp; English.

The present invention describes a method (M1) for designing capture oligonucleotide probes (I) for use on a support to which complementary oligonucleotide probes (II) will hybridise with little mismatch, where (i) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenzae, fungal infectious agents e.g. Cryptococcus neoformans, Candida albicans and Aspergillus fumigatus, viruses e.g. T-cell lymphocytopathic virus, Epstein-Barr virus and polio virus, and parasitic infectious agents selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus medinensis. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects. Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCA1 gene, p53 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. AB182074 to AB197546 represent oligonucleotide sequences used in the exemplification of the present invention.

SQ Sequence 24 BP; 7 A; 6 C; 8 G; 3 T; 0 other;

Oy Query Match 60.9%; Score 13.4; DB 24; Length 24;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

D8 8 CGATATGCGTCTCAG 22
 |||||
D20 CCATATGGTCGTACG 6

RESULT 17
AAX04272
ID AAX04272 standard; DNA; 36 BP.
XX AAX04272;
DT 15-APR-1999 (first entry)
XX HAV-A linker regions of PAP-257.
KX Ricin-like toxin; cancer; viral infection; parasitic infection;
KW linker; B chain; A chain; protease; fungal infection; malaria;
KM leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
KN rhinovirus; laryngotracheitis; poliomyelitis; varicella zoster;
KM cystic fibrosis; multiple sclerosis; ds.
OS Hepatitis A virus.
OS Synthetic.
EN MO9849311-AAZ.
PD 05-NOV-1998.
PF 30-APR-1998; 98MO-CA00394.
PR 29-OCT-1997; 97US-0063715.
PA 30-APR-1997; 97US-0045148.
PI (DNOV-) DE NOVO ENZYME CORP.
PT Borgford T;
DR WPI; 1999-009431/01.
WT New nucleic acid encoding ricin-like toxin with an interchain linker

PT cleaved by protease - is specific for diseased cells, useful for,
 XX e.g. killing selectively cancer or infected cells
 PS Disclosure; Fig 23B; 352pp; English.

XX The present invention describes new purified and isolated nucleic acids
 CC (1) encoding: (i) the A and B chains of a ricin-like toxin (ii); and
 CC (ii) a heterologous linker, joining the two chains and including a
 CC cleavage recognition site for a disease-specific protease (iii). Also
 CC described are: (1) plasmids or baculovirus transfer vectors that contain
 CC (1); and (2) recombinant protein (iv) consisting of the A and B chains
 CC of (ii) joined by the specified linker. (iv), produced by expression of
 CC (1) in host cells, are used to inhibit or kill diseased cells that
 CC produce (iii), particularly for treating cancers (e.g. leucocyte
 CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
 CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
 CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis,
 CC poliomyelitis or varicella zoster), also cystic fibrosis and multiple
 CC sclerosis. Alternatively, (i) is used to express (iv) in vivo. (iv) is
 CC toxic specifically for (iii)-expressing cells and does not depend for
 CC specificity on a cell-binding component. When used to treat virus-
 CC infected cells, transcytosis and cytotoxicity of (iv) are increased by
 CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
 CC some viruses exploit to avoid immune detection), so selectivity and
 CC safety are further improved. (iv) are not toxic until chain A is
 CC released and this occurs only in target cells. The present sequence
 CC represents a nucleotide sequence from the present invention.

XX Sequence 36 BP; 11 A; 7 C; 7 G; 11 T; 0 other;

Query Match 59.1%; Score 13; DB 20; Length 36;
 Best Local Similarity 76.2%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCA 21
 |||||
 DB 7 CTTAGAACGCAATCGTCTCA 27

RESULT 18
 AAX04272/c
 ID AAX04272 standard; DNA; 36 BP.
 XX
 AC AAX04272;

DT 15-APR-1999 (first entry)

DE HAV-A linker regions of pap-257.

XX Ricin-like toxin; cancer; viral infection; parasitic infection;
 KM linker; B chain; A chain; protease; fungal infection; malaria;
 KM leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
 KM rhinovirus; laryngeotracheitis; poliomyelitis; varicella zoster;
 KM cystic fibrosis; multiple sclerosis; ds.

XX Hepatitis A virus.
 OS Synthetic.

PN W09849311-A2.

PD 05-NOV-1998.

PF 30-APR-1998; 98WO-CA00394.

PR 29-OCT-1997; 97US-0063715.

PA 30-APR-1997; 97US-0045148.

PA (DNOV-) DE NOVO ENZYME CORP.

PI Borgford T;

WPI; 1999-009431/01.

PT New nucleic acid encoding ricin-like toxin with an interchain linker
 XX cleaved by protease - is specific for diseased cells, useful for,
 PT e.g. killing selectively cancer or infected cells
 PS Disclosure; Fig 23B; 352pp; English.

XX The present invention describes new purified and isolated nucleic acids
 CC (1) encoding: (i) the A and B chains of a ricin-like toxin (ii); and
 CC (ii) a heterologous linker, joining the two chains and including a
 CC cleavage recognition site for a disease-specific protease (iii). Also
 CC described are: (1) plasmids or baculovirus transfer vectors that contain
 CC (1); and (2) recombinant protein (iv) consisting of the A and B chains
 CC of (ii) joined by the specified linker. (iv), produced by expression of
 CC (1) in host cells, are used to inhibit or kill diseased cells that
 CC produce (iii), particularly for treating cancers (e.g. leucocyte
 CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
 CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
 CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis,
 CC poliomyelitis or varicella zoster), also cystic fibrosis and multiple
 CC sclerosis. Alternatively, (i) is used to express (iv) in vivo. (iv) is
 CC toxic specifically for (iii)-expressing cells and does not depend for
 CC specificity on a cell-binding component. When used to treat virus-
 CC infected cells, transcytosis and cytotoxicity of (iv) are increased by
 CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
 CC some viruses exploit to avoid immune detection), so selectivity and
 CC safety are further improved. (iv) are not toxic until chain A is
 CC released and this occurs only in target cells. The present sequence
 CC represents a nucleotide sequence from the present invention.

XX Sequence 36 BP; 11 A; 7 C; 7 G; 11 T; 0 other;

Query Match 59.1%; Score 13; DB 20; Length 36;
 Best Local Similarity 76.2%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGTCTCAG 22
 |||||
 DB 27 TGAGAACGCAATCGTCTCAG 7

RESULT 19
 AAT78823
 ID AAT78823 standard; DNA; 44 BP.
 XX
 AC AAT78823;

DT 23-JUN-1998 (first entry)

DE Kappa light chain PCR reaction 2 PCR primer O-561.

XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
 KM transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
 KM transplant rejection; immunoglobulin; ss.

XX Synthetic.

OS Homo sapiens.

PN W09713852-A1.

PD 17-APR-1997.

PF 10-OCT-1996; 96WO-US16433.

PR 10-OCT-1995; 95US-0544404.

PA (GENP-) GENPHARM INT INC.

PA Kay RM, Lonberg N;

PI WPI; 1997-235888/21.

PT Novel anti-CD4 antibody produced by transgenic mice - used in the
 PT treatment of auto-immune disease etc.

XX Example 42; Page 266; 396pp; English.
PS A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply
CC 1000000000 M-1 for binding to a predetermined human antigen. The present
CC sequence represents a PCR primer involved in the light chain PCR
CC reaction 2 for the production of a synthetic kappa light chain. Anti-
CC CD4 antibodies may be used in therapeutic and diagnostic applications,
CC especially for the treatment of human diseases. These antibodies reduce
CC activity of CD4 cells and reduce undesirable autoimmune reactions,
CC inflammatory response and transplant rejection. Transgenic animals are
CC capable of producing heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. These animals produce a first Ig type
CC that is necessary for antigen-stimulated B-cell maturation and can
CC switch to encode and produce one or more subsequent heterologous
CC isotypes.
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;
XX
XX
Query Match 59.1%; Score 13; DB 18; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 TGAGACCGATATCGTCTCAG 22
Db 9 TGAGAGTGAATCTGTCCAG 29
RESULT 20
AAAT78823/c
ID AAAT78823 standard; DNA; 44 BP.
XX
XX AAAT78823;
AC
XX 23-JAN-1998 (first entry)
XX
XX
DE Kappa light chain PCR reaction 2 PCR primer O-561.
XX
XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW transplant rejection; immunoglobulin; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9713852-A1.
XX
XX 17-APR-1997.
XX
XX PF 10-OCT-1996; 96WO-US16433.
XX
XX PR 10-OCT-1995; 95US-0544404.
XX
XX (GENP-) GENPHARM INT. INC.
XX
XX PI Kay RM, Lonberg N;
XX
XX WPI; 1997-235888/21.
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
XX
PS Example 42; Page 266; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply
CC 1000000000 M-1 for binding to a predetermined human antigen. The present
CC sequence represents a PCR primer involved in the light chain PCR
CC reaction 2 for the production of a synthetic kappa light chain. Anti-
CC CD4 antibodies may be used in therapeutic and diagnostic applications,
CC especially for the treatment of human diseases. These antibodies reduce
CC activity of CD4 cells and reduce undesirable autoimmune reactions,

CC inflammatory response and transplant rejection. Transgenic animals are
CC capable of producing heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. These animals produce a first Ig type
CC that is necessary for antigen-stimulated B-cell maturation and can
CC switch to encode and produce one or more subsequent heterologous
CC isotypes.
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;
XX
XX
Query Match 59.1%; Score 13; DB 18; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CTGAGACCGATATCGTCTCA 21
Db 29 CTGGACACATTTCACTCTCA 9
RESULT 21
AAV39264
ID AAV39264 standard; DNA; 44 BP.
XX
XX AAV39264;
AC
XX 18-DEC-1998 (first entry)
XX
XX
DE Primer O-561 used to make a synthetic kappa light chain.
XX
XX Transgenic animal; human heterologous antibody; transgene;
KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW autoimmune reaction; inflammatory response; transplant rejection;
KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9824884-A1.
XX
XX
XX 11-JUN-1998.
XX
XX PF 01-DEC-1997; 97WO-US21803.
XX
XX PR 02-DEC-1996; 96US-0758417.
XX
XX (GENP-) GENPHARM INT.
XX
XX PI Kay RM, Lonberg N;
XX
XX WPI; 1998-333306/29.
XX
XX Hybridoma producing antibody specific for interleukin-8 - used to
PT prevent efflux of neutrophils from vasculature, and treat
PT reperfusion injury
XX
XX
PS Example 42; Page 317; 452pp; English.
XX
XX Oligonucleotides AAV39256-64 were used to create a synthetic kappa light
CC chain. Oligonucleotides AAV39256-64 were pooled, and amplified with the
CC AAV39248 and AAV39265. The amplification product was combined with the
CC product of oligonucleotides AAV39244-53, and then amplified. The sequence
CC was then cloned into a vector, which is used to produce the transgenic
CC mouse of the invention. The specification describes transgenic non-human
CC animals, especially a mouse, which are capable of producing a human
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. The transgenic animals have human heavy and light chain
CC transgenes. The transgenes are capable of functionally rearranging a
CC heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)
CC recombination. The transgenes include a heavy chain transgene comprising
CC at least one V, D and J gene segment, and one constant region gene
CC segment. The immunoglobulin (Ig) light chain transgene comprises at
CC least one V and J gene segment and one constant region gene segment. The
CC gene segments are heterologous to the transgenic animal. The antibody can

CC be used to prevent efflux of neutrophils from vasculature. It can also
CC be used to treat reperfusion injury. CD4 binding antibodies are used to
CC reduce undesirable autoimmune reactions, inflammatory responses and
CC rejection of transplanted organs. The anti-IL-8 antibodies can reduce
CC tissue damage and prolong survival in animal models of acute adult
CC respiratory distress syndrome (ARDS) and acid induced lung injury. The
CC anti-IL-8 antibodies can also be used for the treatment of vasculitis,
CC septic shock, allergic reactions (e.g. asthma) and cystic fibrosis.
XX
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;
XX
Query Match 59.1%; Score 13; DB 19; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGGTCTCAG 22
DB 9 TGAGAGTGAAATCTGTCCAG 29
RESULT 22
AAV39264/C
ID AAV39264 standard; DNA; 44 BP.
XX
AC AAV39264;
XX
DT 18-DEC-1998 (first entry)
XX
DE Primer 0-561 used to make a synthetic kappa light chain.
XX
XX Transgenic animal; human heterologous antibody; transgene;
KM isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KM autoimmune reaction; inflammatory response; transplant rejection;
KM acid induced lung injury; acute adult respiratory distress syndrome;
KM ARDS; vasculitis; septic shock; allergic reaction; asthma;
KM cystic fibrosis; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9824884-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US21803.
XX
PR 02-DEC-1996; 96US-0758417.
XX
XX (GENP-) GENPHARM INT.
PA
PI Kay RM, Lonberg N;
XX
XX WPI; 1998-333306/29.
DR
XX Hybridoma producing antibody specific for interleukin-8 - used to
PT prevent efflux of neutrophils from vasculature, and treat
PT reperfusion injury
XX
PS Example 42; Page 317; 452pp; English.
XX
CC Oligonucleotides AAV39256-64 were used to create a synthetic kappa light
CC chain. Oligonucleotides AAV39256-64 were pooled, and amplified with
CC AAV39248 and AAV39265. The amplification product was combined with the
CC product of oligonucleotides AAV39244-53, and then amplified. The sequence
CC was then cloned into a vector, which is used to produce the transgene
CC mouse of the invention. The specification describes transgenic non-human
CC animals, especially a mouse, which are capable of producing a human
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. The transgenic animals have human heavy and light chain
CC transgenes. The transgenes are capable of functionally rearranging a
CC heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)
CC recombination. The transgenes include a heavy chain transgene comprising
CC at least one V, D and J gene segment, and one constant region gene
CC segment. The immunoglobulin (Ig) light chain transgene comprises at

CC least one V and J gene segment and one constant region gene segment. The
CC gene segments are heterologous to the transgenic animal. The antibody can
CC be used to prevent efflux of neutrophils from vasculature. It can also
CC be used to treat reperfusion injury. CD4 binding antibodies are used to
CC reduce undesirable autoimmune reactions, inflammatory responses and
CC rejection of transplanted organs. The anti-IL-8 antibodies can reduce
CC tissue damage and prolong survival in animal models of acute adult
CC respiratory distress syndrome (ARDS) and acid induced lung injury. The
CC anti-IL-8 antibodies can also be used for the treatment of vasculitis,
CC septic shock, allergic reactions (e.g. asthma) and cystic fibrosis.
XX
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;
XX
Query Match 59.1%; Score 13; DB 19; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGTCTCA 21
DB 29 CTGGAGAGATTCTCACTCA 9
RESULT 23
AAZ22018
ID AAZ22018 standard; DNA; 44 BP.
XX
AC AAZ22018;
XX
DT 24-NOV-1999 (first entry)
XX
XX Oligonucleotide used for minigene construction.
DE
XX Transgenic animal; heterologous antibody; hybridoma; B cell;
KM transgenic mouse; human heavy chain transgene; digoxin;
KM human light chain transgene; immortalized cell; immunoglobulin;
KM Shiga-like toxin; autoimmune disease; cancer; infectious disease;
KM transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS Synthetic.
XX
PN WO9945962-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05535.
XX
PR 13-MAR-1998; 98US-0042353.
XX
XX (GENP-) GENPHARM INT INC.
PA
PI Lonberg N, Fishwild DM, Ball WJ;
XX
XX WPI; 1999-551219/46.
DR
XX Novel transgenic non-human animals used to produce heterologous
PT antibodies
PT
PS Example 42; Page 318; 484pp; English.
XX
XX The specification describes transgenic animals that are capable of
CC producing a heterologous antibody. The antibodies are isolated from a
CC hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC having a genome comprising a human heavy chain transgene and a human
CC light chain transgene. The B cells are fused to immortalized cells
CC suitable for generating a hybridoma, which produces a detectable
CC amount of an immunoglobulin that specifically binds digoxin or
CC Shiga-like toxin. B cells from transgenic animals can be used to
CC generate hybridomas expressing monoclonal high affinity human sequence
CC antibodies. Antibodies produced from the transgenic animals of the
CC invention can be used to treat human diseases, e.g. autoimmune
CC diseases, cancer, infectious disease, transplant rejection, blood
CC disorders such as coagulation disorders and other diseases. The
CC present sequence is used in the course of the invention.

RESULT 26

AA243102/c
ID AA243102 standard; DNA; 24 BP.
XX
XX
AC AA243102;
XX
DT 04-FEB-2000 (first entry)
XX
DE PCR primer for C. elegans insulin-like protein ZK84.6.
XX
XX Insulin-like protein; diagnosis; insulin-like gene analysis; nematode;
KM insulin hormone; aging; senescence; pesticide target; signalling pathway;
KM signal transduction pathway; PCR primer; ss.
XX
OS Synthetic.
OS Caenorhabditis elegans.
XX
XX WO954436-A2.
XX
PN 28-OCT-1999.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US08522.
XX
XX 17-APR-1998; 98US-0062580.
PR 08-MAY-1998; 98US-0074984.
PR 26-MAY-1998; 98US-0084303.
XX
XX (EXEL-) EXELIXIS PHARM INC.
XX
XX Homburger SA, Platt DM, Ferguson KC, Doberstein SK, Buchman AR;
PI Reddy BP;
XX
XX WPI; 2000-013239/01.
XX
PT Analysing Caenorhabditis elegans insulin-like gene expression, nucleic
PT acids and proteins of the C. elegans insulin-like genes -
XX
XX Example 1; Page 45; 194pp; English.
XX
XX This sequence represents a PCR primer for DNA encoding a Caenorhabditis
CC elegans insulin-like protein. The amplified sequence can be used in the
CC method of the invention, for analysing an effect of expression or
CC mis-expression of a C. elegans insulin-like gene, which comprises
CC observing a first nematode genetically engineered to express or
CC mis-express a C. elegans insulin-like protein (ILP) of any one of groups
CC 1, II or IV or a derivative or fragment that displays one or more
CC functional activities of the C. elegans ILP. The insulin-like genes in
CC C. elegans constitute very useful tools for probing the function and
CC regulation of their corresponding pathways. This can be expected to lead
CC to the discovery of new drug targets, therapeutic proteins, diagnostics
CC and prognostics useful in the treatment of diseases and clinical problems
CC associated with the function of insulin hormones in humans and other
CC animals, as well as clinical problems associated with aging and
CC senescence. The information may also be useful in identification and
CC validation of pesticide targets in invertebrate pests that are components
CC of these signalling pathways. The genes are also useful for identifying
CC factors that are upstream of the receptor in the signal transduction
CC pathway. The ligand-encoding C. elegans insulin-like genes provide a
CC superior approach for identifying factors that are upstream of the
CC receptor in the signal transduction pathway.
XX
XX Sequence 24 BP; 7 A; 3 C; 8 G; 6 T; 0 other;

Query Match 58.2%; Score 12.8; DB 21; Length 24;

Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CCGATATCGTCTCAG 22
DB 24 CCGATATCGTCTCTG 9

RESULT 27

AA289641
ID AA289641 standard; DNA; 34 BP.
XX
XX
AC AA289641;
XX
DT 28-JUN-2000 (first entry)
XX
DE Plasmid pUC19 primer 1.
XX
XX Primer; pUC19; screening; polymorphism; mutation; ss.
KM
XX
OS Synthetic.
OS
XX WO200014282-A1.
XX
PN 16-MAR-2000.
XX
PD 31-AUG-1999; 99WO-US20047.
XX
PF 04-SEP-1998; 98US-0099147.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Brenner S;
XX
XX WPI; 2000-257018/22.
XX
DR Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form
PT amplicons -
XX
XX
XX Disclosure; Page 24; 27pp; English.
XX
XX This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AA289641-289646 represent the primers used in the method of the
CC invention.
XX
XX Sequence 34 BP; 8 A; 9 C; 9 G; 8 T; 0 other;

Query Match 58.2%; Score 12.8; DB 21; Length 34;
Best Local Similarity 87.5%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGACCGATATCGTCT 19
DB 12 AGACCGATATCGTCT 27

RESULT 28

AA289641/c
ID AA289641 standard; DNA; 34 BP.
XX
XX
AC AA289641;
XX
DT 28-JUN-2000 (first entry)
XX
XX Plasmid pUC19 primer 1.
DE
XX
XX Primer; pUC19; screening; polymorphism; mutation; ss.
KM
XX
OS Synthetic.
OS
XX WO200014282-A1.
XX
PN 16-MAR-2000.
XX

QY 7 CCGATATCGTCTCAG 22
DB 24 CCGATATCGTCTCTG 9

QY 4 AGACCGATATCGTCT 19
||| ||||| |||
Db 27 AGACCGATATCGTCT 12

RESULT 31
ID AAI66435 standard; DNA; 41 BP.
XX AAI66435;
AC AAI66435;

XX 04-DEC-2001 (first entry)

XX Human thrombotic protein 46 coding sequence probe #2.

XX Human thrombotic protein 46; cancer; HIV infection; gene therapy;

XX probe; ss.

XX Homo sapiens.

XX CNI300774-A.

XX 27-JUN-2001.

XX 22-DEC-1999; 99CN-0125685.

XX 22-DEC-1999; 99CN-0125685.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2001-530462/59.

XX New human thrombotic protein 46 and polynucleotide encoding it, useful
PT for treating cancer and human immunodeficiency virus infection -

XX Example 7; Page 20(Disclosure); 32pp; Chinese.

XX The present invention provides the protein and coding sequences of human

CC thrombotic protein 46. The sequences can be used in the treatment of

CC cancer and HIV infection. The present sequence is a probe for the

CC coding sequence of the invention.

XX Sequence 41 BP; 11 A; 11 C; 9 G; 10 T; 0 other;

Query Match 58.2%; Score 12.8; DB 22; Length 41;
Best Local Similarity 87.5%; Pred. No. 5e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAGACGATATCGGTC 18
||| ||||| ||||| |||

Db 26 GAGACGATATCGTTC 41

RESULT 32
ID AAI66435/c

XX AAI66435 standard; DNA; 41 BP.

XX AAI66435;

XX 04-DEC-2001 (first entry)

XX Human thrombotic protein 46 coding sequence probe #2.

XX Human thrombotic protein 46; cancer; HIV infection; gene therapy;

XX probe; ss.

XX Homo sapiens.

XX CNI300774-A.

XX 27-JUN-2001.

XX 22-DEC-1999; 99CN-0125685.
XX 22-DEC-1999; 99CN-0125685.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2001-530462/59.

XX New human thrombotic protein 46 and polynucleotide encoding it, useful
PT for treating cancer and human immunodeficiency virus infection -

XX Example 7; Page 20(Disclosure); 32pp; Chinese.

XX The present invention provides the protein and coding sequences of human

CC thrombotic protein 46. The sequences can be used in the treatment of

CC cancer and HIV infection. The present sequence is a probe for the

CC coding sequence of the invention.

XX Sequence 41 BP; 11 A; 11 C; 9 G; 10 T; 0 other;

Query Match 58.2%; Score 12.8; DB 22; Length 41;
Best Local Similarity 87.5%; Pred. No. 5e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GACCGATATCGTCTC 20
||| ||||| ||||| |||

Db 41 GACCGATATCGTCTC 26

RESULT 33
ID AA289643 standard; DNA; 43 BP.

XX AA289643;

XX 28-JUN-2000 (first entry)

XX Plasmid pUC19 primer 3.

XX Primer; pUC19; screening; polymorphism; mutation; ss.

XX Synthetic.

XX WO200014282-A1.

XX 31-AUG-1999; 99MO-US20047.

XX 04-SEP-1998; 98US-0099147.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Brenner S;

XX WPI; 2000-257018/22.

XX Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form

XX amplicons -

XX Disclosure; Page 25; 27pp; English.

XX This invention describes a novel method (I) for identifying polymorphic

CC DNA sequences which comprises forming a population of heteroduplexes,

CC isolating and amplifying mismatched heteroduplexes to form amplicons,

CC and determining the sequence of the amplicon. The methods are useful for

CC identifying polymorphic DNA sequences and for comparing a reference DNA

CC population with test populations for identifying sequences that are

CC different (e.g. mutated sequences). The method allows large scale

CC identification of polymorphic or mutated sequences in an individual.
CC AA289641-289646 represent the primers used in the method of the
CC invention.
XX
SQ Sequence 43 BP; 11 A; 10 C; 10 G; 12 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGCTCT 19
DB 18 AGACCGATATCGCTCT 33
RESULT 34
AA289643/C
ID AA289643 standard; DNA; 43 BP.
XX
AC AA289643;
XX
DT 28-JUN-2000 (first entry)
XX
DE Plasmid pUC19 primer 3.
XX
KM Primer; pUC19; screening; polymorphism; mutation; ss.
XX
OS Synthetic.
XX
PN WO200014282-A1.
XX
PD 16-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US20047.
XX
PR 04-SEP-1998; 98US-0099147.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Brenner S;
XX
DR WPI; 2000-257018/22.
XX
PT Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form
PT amplicons -
XX
PS Disclosure; Page 25; 27pp; English.
XX
CC This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AA289641-289646 represent the primers used in the method of the
CC invention.
XX
SQ Sequence 43 BP; 11 A; 10 C; 10 G; 12 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGCTCT 19
DB 33 AGACCGATATCGCTCT 18
RESULT 35
AA289644

ID AA289644 standard; DNA; 43 BP.
XX
AC AA289644;
XX
DT 28-JUN-2000 (first entry)
XX
DE Plasmid pUC19 primer 4.
XX
KM Primer; pUC19; screening; polymorphism; mutation; ss.
XX
OS Synthetic.
XX
PN WO200014282-A1.
XX
PD 16-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US20047.
XX
PR 04-SEP-1998; 98US-0099147.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Brenner S;
XX
DR WPI; 2000-257018/22.
XX
PT Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form
PT amplicons -
XX
PS Disclosure; Page 25; 27pp; English.
XX
CC This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AA289641-289646 represent the primers used in the method of the
CC invention.
XX
SQ Sequence 43 BP; 11 A; 11 C; 11 G; 10 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGCTCT 19
DB 15 AGACCGATATCGCTCT 30
RESULT 36
AA289644/C
ID AA289644 standard; DNA; 43 BP.
XX
AC AA289644;
XX
DT 28-JUN-2000 (first entry)
XX
DE Plasmid pUC19 primer 4.
XX
KM Primer; pUC19; screening; polymorphism; mutation; ss.
XX
OS Synthetic.
XX
PN WO200014282-A1.
XX
PD 16-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US20047.

```
XX 04-SEP-1998; 98US-0099147.
PR (LYNX-) LYNX THERAPEUTICS INC.
PA
XX Brenner S;
XX WPI; 2000-257018/22.
DR
XX Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form
XX amplicons -
PS Disclosure; Page 25; 27pp; English.
XX
CC This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AA289641-289646 represent the primers used in the method of the
CC invention.
XX
SQ Sequence 43 BP; 11 A; 11 C; 11 G; 10 T; 0 other;
XX
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 4 AGACCGATATCGGTCT 19
DB 30 AGACCGATATCGGTCT 15
XX
RESULT 37
ABI90430
ID ABI90430 standard; DNA; 24 BP.
XX
AC ABI90430;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#4017 oligo #1.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
XX WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
```

```
XX The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensic and the food
CC and feed industry, detecting complementary scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;
XX
Query Match 57.3%; Score 12.6; DB 24; Length 24;
Best Local Similarity 78.3%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1 CTGGAGCCGATACGGTCT 19
DB 6 CTGGAGCCGATACGGTCT 24
XX
RESULT 38
ABI90430/C
ID ABI90430 standard; DNA; 24 BP.
XX
AC ABI90430;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#4017 oligo #1.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
XX WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
```

XX The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;
XX
Query Match 57.3%; Score 12.6; DB 24; Length 24;
Best Local Similarity 78.9%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 4 AGACCGATATCGGTCTCAG 22
DB 24 AGACCGATATCGGTCTCAG 6
XX
RESULT 39
AB190431
ID AB190431 standard; DNA; 24 BP.
XX
AC AB190431;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#4017 oligo #2.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture
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CC oligonucleotide probes (II) will hybridise with little mismatch, where
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CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
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CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
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CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;
XX
Query Match 57.3%; Score 12.6; DB 24; Length 24;
Best Local Similarity 78.9%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 4 AGACCGATATCGGTCTCAG 22
DB 1 AGACCGATATCGGTCTCAG 19
XX
RESULT 40
AB190431/c
ID AB190431 standard; DNA; 24 BP.
XX
AC AB190431;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#4017 oligo #2.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture
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 CC oligonucleotide probes (II) will hybridise with little mismatch, where
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 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;

Query Match 57.3%; Score 12.6; DB 24; Length 24;
 Best Local Similarity 78.9%; Pred. No. 6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACGATATCGGTCT 19
 |||||
 Db 19 CTGGGACCCATACGGGTCT 1

Search completed: June 14, 2003, 21:58:11
 Job time : 218 secs

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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 21:55:20 ; Search time 64 Seconds
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105,420 Million cell updates/sec

Title: US-09-532-001-1
Perfect score: 22
Sequence: 1 CTGAGACCGATATCGGCTCTCAG 22

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
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- 5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	13	59.1	44	4	US-09-042-353-391
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4	13	59.1	44	4	US-08-758-417A-241
5	12.4	56.4	30	1	US-08-235-503B-61
6	12.4	56.4	30	1	US-08-235-503B-61
7	12.4	56.4	30	5	PCT-US95-05265-61
8	12.4	56.4	30	5	PCT-US95-05265-61
9	12.4	56.4	32	2	US-08-956-047-22
10	12.4	56.4	32	2	US-08-956-047-22
11	12.2	55.5	33	1	US-08-447-422-1
12	12.2	55.5	33	1	US-08-447-422-1
13	12.2	55.5	33	3	US-09-213-053-8
14	12.2	55.5	33	3	US-09-213-053-8
15	12.2	55.5	33	3	US-09-213-053-9
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17	12.2	55.5	33	3	US-09-213-053-28
18	12.2	55.5	33	3	US-09-213-053-28
19	12.2	55.5	33	3	US-09-213-053-29
20	12.2	55.5	33	3	US-09-213-053-29
21	12.2	54.5	28	1	US-08-235-503B-68
22	12.2	54.5	28	1	US-08-235-503B-68
23	12.2	54.5	28	1	US-08-235-503B-69
24	12.2	54.5	28	1	US-08-235-503B-69
25	12.2	54.5	28	5	PCT-US95-05265-68
26	12.2	54.5	28	5	PCT-US95-05265-68
27	12.2	54.5	28	5	PCT-US95-05265-69

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C 29	12	54.5	37	1	US-08-402-964-3	Sequence 3, App1
C 30	12	54.5	37	1	US-08-402-964-3	Sequence 3, App1
C 31	12	54.5	47	4	US-09-641-638-720	Sequence 720, App
C 32	12	54.5	47	4	US-09-641-638-720	Sequence 720, App
C 33	11.8	53.6	34	3	US-09-213-053-21	Sequence 21, App1
C 34	11.8	53.6	34	3	US-09-213-053-21	Sequence 21, App1
C 35	11.8	53.6	45	1	US-07-967-693-43	Sequence 43, App1
C 36	11.8	53.6	45	1	US-07-967-693-43	Sequence 43, App1
C 37	11.8	53.6	45	1	US-08-195-072-41	Sequence 41, App1
C 38	11.8	53.6	45	1	US-08-195-072-41	Sequence 41, App1
C 39	11.8	53.6	45	1	US-08-195-733-41	Sequence 41, App1
C 40	11.8	53.6	45	1	US-08-195-733-41	Sequence 41, App1
C 41	11.8	53.6	45	1	US-08-195-747-41	Sequence 41, App1
C 42	11.8	53.6	45	1	US-08-195-747-41	Sequence 41, App1
C 43	11.8	53.6	45	1	US-08-446-884-41	Sequence 41, App1
C 44	11.8	53.6	45	1	US-08-446-884-41	Sequence 41, App1
C 45	11.8	53.6	45	1	US-08-195-073-41	Sequence 41, App1
C 46	11.8	53.6	45	1	US-08-195-073-41	Sequence 41, App1
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C 275	10.4	47.3	29	2	US-08-454-680-3	Sequence 18, Appl1	C 347	10.4	47.3	48	2	US-08-739-167-4	Sequence 4, Appl1
C 276	10.4	47.3	29	2	US-08-454-680-3	Sequence 3, Appl1	C 348	10.4	47.3	48	2	US-08-739-167-4	Sequence 4, Appl1
C 277	10.4	47.3	29	2	US-08-438-562-18	Sequence 3, Appl1	C 349	10.4	47.3	48	3	US-08-739-167-4	Sequence 4, Appl1
C 278	10.4	47.3	29	2	US-08-438-562-18	Sequence 18, Appl1	C 350	10.4	47.3	48	3	US-08-404-796-4	Sequence 4, Appl1
C 279	10.4	47.3	29	2	US-08-483-528B-18	Sequence 18, Appl1	C 351	10.4	47.3	48	3	US-08-404-796-4	Sequence 4, Appl1
C 280	10.4	47.3	29	2	US-08-483-528B-18	Sequence 18, Appl1	C 352	10.4	47.3	48	3	US-08-331-869-4	Sequence 4, Appl1
C 281	10.4	47.3	29	3	US-08-673-799C-18	Sequence 18, Appl1	C 353	10.4	47.3	48	4	US-09-350-399-4	Sequence 4, Appl1
C 282	10.4	47.3	29	3	US-08-673-799C-18	Sequence 18, Appl1	C 354	10.4	47.3	48	4	US-09-350-399-4	Sequence 4, Appl1
C 283	10.4	47.3	29	4	US-09-393-385B-18	Sequence 18, Appl1	C 355	10.4	47.3	48	4	US-09-236-140A-4	Sequence 4, Appl1
C 284	10.4	47.3	29	4	US-09-393-385B-18	Sequence 18, Appl1	C 356	10.4	47.3	48	4	US-09-236-140A-4	Sequence 4, Appl1
C 285	10.4	47.3	29	4	US-09-325-328B-6	Sequence 6, Appl1	C 357	10.4	47.3	48	4	US-09-415-784-12	Sequence 12, Appl1
C 286	10.4	47.3	29	4	US-09-325-328B-6	Sequence 6, Appl1	C 358	10.4	47.3	48	4	US-09-415-784-12	Sequence 12, Appl1
C 287	10.4	47.3	31	1	US-08-482-882-31	Sequence 31, Appl1	C 359	10.4	47.3	48	4	US-09-415-785A-12	Sequence 12, Appl1
C 288	10.4	47.3	31	1	US-08-482-882-31	Sequence 31, Appl1	C 360	10.4	47.3	48	4	US-09-415-785A-12	Sequence 12, Appl1
C 289	10.4	47.3	31	1	US-08-483-389-31	Sequence 31, Appl1	C 361	10.4	47.3	48	4	US-08-944-465-12	Sequence 12, Appl1
C 290	10.4	47.3	31	1	US-08-483-389-31	Sequence 31, Appl1	C 362	10.4	47.3	48	4	US-08-944-465-12	Sequence 12, Appl1
C 291	10.4	47.3	31	2	US-08-487-113D-31	Sequence 31, Appl1	C 363	10.4	47.3	48	4	US-09-415-868-12	Sequence 12, Appl1
C 292	10.4	47.3	31	2	US-08-487-113D-31	Sequence 31, Appl1	C 364	10.4	47.3	48	4	US-09-415-868-12	Sequence 12, Appl1
C 293	10.4	47.3	31	2	US-08-473-503-31	Sequence 31, Appl1	C 365	10.4	47.3	48	4	US-09-415-900-12	Sequence 12, Appl1
C 294	10.4	47.3	31	2	US-08-473-503-31	Sequence 31, Appl1	C 366	10.4	47.3	48	4	US-09-415-900-12	Sequence 12, Appl1
C 295	10.4	47.3	31	2	US-08-318-157B-41	Sequence 41, Appl1	C 367	10.2	46.4	14	1	US-08-309-512-26	Sequence 26, Appl1
C 296	10.4	47.3	31	2	US-08-318-157B-41	Sequence 41, Appl1	C 368	10.2	46.4	14	1	US-08-309-512-26	Sequence 26, Appl1
C 297	10.4	47.3	31	2	US-08-483-932-31	Sequence 31, Appl1	C 369	10.2	46.4	20	2	US-08-500-635A-4	Sequence 4, Appl1
C 298	10.4	47.3	31	2	US-08-483-932-31	Sequence 31, Appl1	C 370	10.2	46.4	20	2	US-08-500-635A-4	Sequence 4, Appl1
C 299	10.4	47.3	31	2	US-08-678-194-1	Sequence 1, Appl1	C 371	10.2	46.4	20	4	US-09-312-183A-18	Sequence 18, Appl1
C 300	10.4	47.3	31	2	US-08-678-194-1	Sequence 1, Appl1	C 372	10.2	46.4	20	4	US-09-312-183A-18	Sequence 18, Appl1
C 301	10.4	47.3	31	2	US-08-720-420A-31	Sequence 31, Appl1	C 373	10.2	46.4	20	4	US-09-167-151-4	Sequence 4, Appl1
C 302	10.4	47.3	31	2	US-08-720-420A-31	Sequence 31, Appl1	C 374	10.2	46.4	20	4	US-09-167-151-4	Sequence 4, Appl1
C 303	10.4	47.3	31	3	US-08-714-017-31	Sequence 31, Appl1	C 375	10.2	46.4	20	4	US-09-360-416-56	Sequence 56, Appl1
C 304	10.4	47.3	31	3	US-08-714-017-31	Sequence 31, Appl1	C 376	10.2	46.4	20	4	US-09-360-416-56	Sequence 56, Appl1
C 305	10.4	47.3	31	3	US-08-475-680-31	Sequence 31, Appl1	C 377	10.2	46.4	23	4	US-09-103-478-11	Sequence 11, Appl1
C 306	10.4	47.3	31	3	US-08-475-680-31	Sequence 31, Appl1	C 378	10.2	46.4	23	4	US-09-103-478-11	Sequence 11, Appl1
C 307	10.4	47.3	31	4	US-08-890-011-1	Sequence 1, Appl1	C 379	10.2	46.4	23	4	US-09-193-931C-11	Sequence 11, Appl1
C 308	10.4	47.3	31	4	US-08-890-011-1	Sequence 1, Appl1	C 380	10.2	46.4	23	4	US-09-193-931C-11	Sequence 11, Appl1
C 309	10.4	47.3	31	4	US-09-171-945-2	Sequence 2, Appl1	C 381	10.2	46.4	24	3	US-09-157-177-51	Sequence 51, Appl1
C 310	10.4	47.3	31	4	US-09-171-945-2	Sequence 2, Appl1	C 382	10.2	46.4	24	3	US-09-157-177-51	Sequence 51, Appl1
C 311	10.4	47.3	31	4	US-09-262-724-1	Sequence 1, Appl1	C 383	10.2	46.4	24	3	US-09-157-177-84	Sequence 84, Appl1
C 312	10.4	47.3	31	4	US-09-262-724-1	Sequence 1, Appl1	C 384	10.2	46.4	24	3	US-09-157-177-84	Sequence 84, Appl1
C 313	10.4	47.3	33	1	US-08-170-290A-39	Sequence 39, Appl1	C 385	10.2	46.4	24	3	US-08-557-006C-10	Sequence 10, Appl1
C 314	10.4	47.3	33	1	US-08-170-290A-39	Sequence 39, Appl1	C 386	10.2	46.4	24	4	US-08-557-006C-10	Sequence 10, Appl1
C 315	10.4	47.3	33	1	US-08-519-103-21	Sequence 21, Appl1	C 387	10.2	46.4	27	1	US-08-447-422-7	Sequence 7, Appl1
C 316	10.4	47.3	33	1	US-08-519-103-21	Sequence 21, Appl1	C 388	10.2	46.4	27	1	US-08-447-422-7	Sequence 7, Appl1
C 317	10.4	47.3	33	4	US-09-018-635-21	Sequence 21, Appl1	C 389	10.2	46.4	29	4	US-09-001-472-6	Sequence 6, Appl1
C 318	10.4	47.3	33	4	US-09-018-635-21	Sequence 21, Appl1	C 390	10.2	46.4	29	4	US-09-001-472-6	Sequence 6, Appl1
C 319	10.4	47.3	36	2	US-08-418-085-24	Sequence 24, Appl1	C 391	10.2	46.4	30	2	US-08-491-988-18	Sequence 18, Appl1
							C 392	10.2	46.4	30	2	US-08-491-988-18	Sequence 18, Appl1

C 393	10.2	46.4	30	3	US-09-078-670-10	Sequence 10, Appl	C 466	10.2	46.4	50	2	US-08-475-228A-586	Sequence 586, App
C 394	10.2	46.4	30	3	US-09-078-670-10	Sequence 10, Appl	C 467	10.2	46.4	50	3	US-08-482-080A-586	Sequence 586, App
C 395	10.2	46.4	30	3	US-09-182-859-29	Sequence 29, Appl	C 468	10.2	46.4	50	3	US-08-482-080A-586	Sequence 586, App
C 396	10.2	46.4	30	3	US-09-182-859-29	Sequence 29, Appl	C 469	10.2	46.4	50	4	US-09-354-947-586	Sequence 586, App
C 397	10.2	46.4	30	4	US-09-426-332-3	Sequence 3, Appl1	C 470	10.2	46.4	50	4	US-09-354-947-586	Sequence 586, App
C 398	10.2	46.4	30	4	US-09-426-332-3	Sequence 3, Appl1	C 471	10.2	46.4	50	5	PCT-US93-12388-586	Sequence 586, App
C 399	10.2	46.4	30	4	US-09-537-168-28	Sequence 28, Appl	C 472	10.2	46.4	50	5	PCT-US93-12388-586	Sequence 586, App
C 400	10.2	46.4	30	4	US-09-537-168-28	Sequence 28, Appl	C 473	10.2	46.4	18	4	US-09-058-847A-7	Sequence 7, Appl1
C 401	10.2	46.4	30	4	US-09-627-154-10	Sequence 10, Appl	C 474	10	45.5	18	4	US-08-974-102-19	Sequence 19, Appl1
C 402	10.2	46.4	30	4	US-09-627-154-10	Sequence 10, Appl	C 475	10	45.5	19	4	US-08-997-251-15	Sequence 15, Appl1
C 403	10.2	46.4	30	4	US-09-672-459-29	Sequence 29, Appl	C 476	10	45.5	19	4	US-08-997-251-15	Sequence 15, Appl1
C 404	10.2	46.4	30	4	US-09-672-459-29	Sequence 29, Appl	C 477	10	45.5	20	2	US-08-680-326-19	Sequence 19, Appl1
C 405	10.2	46.4	33	1	US-08-438-639-46	Sequence 46, Appl	C 478	10	45.5	20	2	US-08-680-326-19	Sequence 19, Appl1
C 406	10.2	46.4	33	1	US-08-438-639-46	Sequence 46, Appl	C 479	10	45.5	21	3	US-08-987-326-18	Sequence 18, Appl1
C 407	10.2	46.4	33	1	US-07-813-388A-46	Sequence 46, Appl	C 480	10	45.5	21	3	US-08-987-326-18	Sequence 18, Appl1
C 408	10.2	46.4	33	1	US-07-813-388A-46	Sequence 46, Appl	C 481	10	45.5	23	4	US-08-781-420-19	Sequence 19, Appl1
C 409	10.2	46.4	33	2	US-08-470-124-79	Sequence 79, Appl	C 482	10	45.5	23	4	US-08-781-420-19	Sequence 19, Appl1
C 410	10.2	46.4	33	2	US-08-470-124-79	Sequence 79, Appl	C 483	10	45.5	23	4	US-08-874-102-19	Sequence 19, Appl1
C 411	10.2	46.4	33	3	US-08-441-971-122	Sequence 122, Appl	C 484	10	45.5	23	4	US-08-874-102-19	Sequence 19, Appl1
C 412	10.2	46.4	33	3	US-08-441-971-122	Sequence 122, Appl	C 485	10	45.5	23	4	US-08-984-919A-19	Sequence 19, Appl1
C 413	10.2	46.4	33	4	US-08-221-653-122	Sequence 122, Appl	C 486	10	45.5	23	4	US-08-984-919A-19	Sequence 19, Appl1
C 414	10.2	46.4	33	4	US-08-221-653-122	Sequence 122, Appl	C 487	10	45.5	23	4	US-09-006-595A-19	Sequence 19, Appl1
C 415	10.2	46.4	33	4	US-08-442-144A-122	Sequence 122, Appl	C 488	10	45.5	23	4	US-09-006-595A-19	Sequence 19, Appl1
C 416	10.2	46.4	33	4	US-08-442-144A-122	Sequence 122, Appl	C 489	10	45.5	24	1	US-08-155-171B-22	Sequence 22, Appl1
C 417	10.2	46.4	33	4	US-08-441-970-122	Sequence 122, Appl	C 490	10	45.5	24	1	US-08-155-171B-22	Sequence 22, Appl1
C 418	10.2	46.4	33	4	US-08-441-970-122	Sequence 122, Appl	C 491	10	45.5	24	2	US-08-435-998-22	Sequence 22, Appl1
C 419	10.2	46.4	34	3	US-08-787-091-12	Sequence 12, Appl	C 492	10	45.5	24	2	US-08-435-998-22	Sequence 22, Appl1
C 420	10.2	46.4	34	3	US-08-787-091-12	Sequence 12, Appl	C 493	10	45.5	24	2	US-08-535-276-13	Sequence 22, Appl1
C 421	10.2	46.4	36	1	US-08-402-964-1	Sequence 1, Appl1	C 494	10	45.5	24	2	US-08-535-276-13	Sequence 22, Appl1
C 422	10.2	46.4	36	1	US-08-402-964-1	Sequence 1, Appl1	C 495	10	45.5	24	2	US-08-535-276-13	Sequence 22, Appl1
C 423	10.2	46.4	36	1	US-08-291-932A-627	Sequence 627, Appl	C 496	10	45.5	24	4	US-09-257-584-26	Sequence 26, Appl1
C 424	10.2	46.4	36	1	US-08-291-932A-627	Sequence 627, Appl	C 497	10	45.5	24	4	US-09-335-234-13	Sequence 13, Appl1
C 425	10.2	46.4	36	1	US-08-334-847-229	Sequence 229, Appl	C 498	10	45.5	25	2	US-08-335-234-13	Sequence 13, Appl1
C 426	10.2	46.4	36	1	US-08-334-847-229	Sequence 229, Appl	C 499	10	45.5	25	2	US-08-155-171B-29	Sequence 29, Appl1
C 427	10.2	46.4	36	1	US-08-334-847-763	Sequence 763, Appl	C 500	10	45.5	25	1	US-08-155-171B-29	Sequence 29, Appl1
C 428	10.2	46.4	36	1	US-08-334-847-763	Sequence 763, Appl	C 501	10	45.5	25	1	US-08-378-588-18	Sequence 18, Appl1
C 429	10.2	46.4	36	1	US-08-363-240A-340	Sequence 340, Appl	C 502	10	45.5	25	1	US-08-378-588-18	Sequence 18, Appl1
C 430	10.2	46.4	36	1	US-08-363-240A-340	Sequence 340, Appl	C 503	10	45.5	25	2	US-08-811-094-18	Sequence 18, Appl1
C 431	10.2	46.4	36	1	US-08-363-240A-347	Sequence 347, Appl	C 504	10	45.5	25	2	US-08-811-094-18	Sequence 18, Appl1
C 432	10.2	46.4	36	1	US-08-363-240A-347	Sequence 347, Appl	C 505	10	45.5	25	2	US-08-435-998-29	Sequence 29, Appl1
C 433	10.2	46.4	37	4	US-09-477-924-5	Sequence 5, Appl1	C 506	10	45.5	25	2	US-08-435-998-29	Sequence 29, Appl1
C 434	10.2	46.4	37	4	US-09-477-924-5	Sequence 5, Appl1	C 507	10	45.5	25	4	US-09-102-831-7	Sequence 7, Appl1
C 435	10.2	46.4	38	1	US-08-373-124A-1324	Sequence 1324, Ap	C 508	10	45.5	25	4	US-09-102-831-7	Sequence 7, Appl1
C 436	10.2	46.4	38	1	US-08-373-124A-1324	Sequence 1324, Ap	C 509	10	45.5	25	4	US-09-102-831-8	Sequence 8, Appl1
C 437	10.2	46.4	38	1	US-08-435-628-1324	Sequence 1324, Ap	C 510	10	45.5	25	4	US-09-102-831-8	Sequence 8, Appl1
C 438	10.2	46.4	38	1	US-08-435-628-1324	Sequence 1324, Ap	C 511	10	45.5	25	4	US-09-102-831-9	Sequence 9, Appl1
C 439	10.2	46.4	38	3	US-09-182-859-28	Sequence 28, Appl	C 512	10	45.5	25	4	US-09-102-831-9	Sequence 9, Appl1
C 440	10.2	46.4	38	3	US-09-182-859-28	Sequence 28, Appl	C 513	10	45.5	25	4	US-09-102-831-10	Sequence 10, Appl1
C 441	10.2	46.4	38	4	US-09-537-168-27	Sequence 27, Appl	C 514	10	45.5	25	4	US-09-102-831-10	Sequence 10, Appl1
C 442	10.2	46.4	38	4	US-09-537-168-27	Sequence 27, Appl	C 515	10	45.5	25	5	PCT-US94-11121-18	Sequence 18, Appl1
C 443	10.2	46.4	38	4	US-09-672-459-28	Sequence 28, Appl	C 516	10	45.5	25	5	PCT-US94-11121-18	Sequence 18, Appl1
C 444	10.2	46.4	38	4	US-09-672-459-28	Sequence 28, Appl	C 517	10	45.5	26	2	US-08-770-565-15	Sequence 15, Appl1
C 445	10.2	46.4	38	4	US-09-375-318-7	Sequence 7, Appl1	C 518	10	45.5	26	2	US-08-770-565-15	Sequence 15, Appl1
C 446	10.2	46.4	38	4	US-09-375-318-7	Sequence 7, Appl1	C 519	10	45.5	26	3	US-08-974-180-21	Sequence 21, Appl1
C 447	10.2	46.4	39	3	US-08-845-546-22	Sequence 22, Appl	C 520	10	45.5	26	3	US-08-974-180-21	Sequence 21, Appl1
C 448	10.2	46.4	39	3	US-08-845-546-22	Sequence 22, Appl	C 521	10	45.5	27	1	US-08-363-585-19	Sequence 19, Appl1
C 449	10.2	46.4	39	6	5256648-22	Patent No. 5256648	C 522	10	45.5	27	1	US-08-363-585-19	Sequence 19, Appl1
C 450	10.2	46.4	39	6	5256648-22	Patent No. 5256648	C 523	10	45.5	27	1	US-08-363-585-20	Sequence 20, Appl1
C 451	10.2	46.4	40	4	US-09-171-025-17	Sequence 17, Appl	C 524	10	45.5	27	1	US-08-363-585-20	Sequence 20, Appl1
C 452	10.2	46.4	40	4	US-09-171-025-17	Sequence 17, Appl	C 525	10	45.5	27	1	US-08-363-585-22	Sequence 22, Appl1
C 453	10.2	46.4	43	1	US-08-720-899-24	Sequence 24, Appl	C 526	10	45.5	27	1	US-08-363-585-22	Sequence 22, Appl1
C 454	10.2	46.4	43	1	US-08-720-899-24	Sequence 24, Appl	C 527	10	45.5	27	4	US-08-584-040-3355	Sequence 3355, Ap
C 455	10.2	46.4	43	1	US-08-459-610-24	Sequence 24, Appl	C 528	10	45.5	27	4	US-08-584-040-3355	Sequence 3355, Ap
C 456	10.2	46.4	43	1	US-08-459-610-24	Sequence 24, Appl	C 529	10	45.5	27	4	US-08-584-040-3355	Sequence 3355, Ap
C 457	10.2	46.4	43	2	US-08-343-804-24	Sequence 24, Appl	C 530	10	45.5	27	4	US-08-584-040-6375	Sequence 6375, Ap
C 458	10.2	46.4	43	2	US-08-343-804-24	Sequence 24, Appl	C 531	10	45.5	27	4	US-08-584-040-6375	Sequence 6375, Ap
C 459	10.2	46.4	44	1	US-08-452-083-27	Sequence 27, Appl	C 532	10	45.5	27	4	US-08-679-645-1103	Sequence 1103, Ap
C 460	10.2	46.4	44	1	US-08-452-083-27	Sequence 27, Appl	C 533	10	45.5	28	3	US-08-974-180-6	Sequence 6, Appl1
C 461	10.2	46.4	50	1	US-08-171-389-586	Sequence 586, App	C 534	10	45.5	28	3	US-08-974-180-6	Sequence 6, Appl1
C 462	10.2	46.4	50	1	US-08-171-389-586	Sequence 586, App	C 535	10	45.5	29	3	US-08-824-692-18	Sequence 18, Appl1
C 463	10.2	46.4	50	1	US-08-123-936-586	Sequence 586, App	C 536	10	45.5	29	3	US-08-824-692-18	Sequence 18, Appl1
C 464	10.2	46.4	50	1	US-08-123-936-586	Sequence 586, App	C 537	10	45.5	29	4	US-09-183-412-36	Sequence 36, Appl1
C 465	10.2	46.4	50	2	US-08-475-228A-586	Sequence 586, App	C 538	10	45.5	29	4	US-09-183-412-36	Sequence 36, Appl1

539	10	45.5	30	4	US-09-230-405-15	Sequence 15, Appl	C 612	10	45.5	41	1	US-08-172-328-11	Sequence 11, Appl
C 540	10	45.5	30	4	US-09-230-405-15	Sequence 15, Appl	613	10	45.5	41	1	US-08-593-535-27	Sequence 27, Appl
C 541	10	45.5	31	4	US-08-679-645-359	Sequence 359, App	C 614	10	45.5	41	1	US-08-593-535-27	Sequence 27, Appl
C 542	10	45.5	31	4	US-08-679-645-359	Sequence 359, App	615	10	45.5	42	2	US-08-880-557-17	Sequence 17, Appl
C 543	10	45.5	31	4	US-09-383-143-50	Sequence 50, Appl	C 616	10	45.5	42	2	US-08-880-557-17	Sequence 17, Appl
C 544	10	45.5	31	4	US-09-383-143-50	Sequence 50, Appl	617	10	45.5	42	2	US-09-189-583-17	Sequence 17, Appl
C 545	10	45.5	32	2	US-08-002-324-6	Sequence 6, Appl1	C 618	10	45.5	42	3	US-09-189-583-17	Sequence 17, Appl
C 546	10	45.5	32	2	US-08-002-324-6	Sequence 6, Appl1	619	10	45.5	42	3	US-09-189-583-17	Sequence 17, Appl
C 547	10	45.5	32	5	PCT-US94-00261-6	Sequence 6, Appl1	C 620	10	45.5	42	4	US-09-402-631A-35	Sequence 35, Appl
C 548	10	45.5	32	5	PCT-US94-00261-6	Sequence 6, Appl1	621	10	45.5	44	1	US-08-592-406-5	Sequence 5, Appl1
C 549	10	45.5	33	1	US-08-212-372-7	Sequence 7, Appl1	C 622	10	45.5	44	1	US-08-592-406-5	Sequence 5, Appl1
C 550	10	45.5	33	1	US-08-212-372-7	Sequence 7, Appl1	623	10	45.5	45	4	US-09-363-970-26	Sequence 26, Appl
C 551	10	45.5	33	2	US-08-343-443B-73	Sequence 73, Appl	C 624	10	45.5	45	4	US-09-363-970-26	Sequence 26, Appl
C 552	10	45.5	33	2	US-08-343-443B-73	Sequence 73, Appl	625	10	45.5	47	1	US-08-340-820-26	Sequence 26, Appl
C 553	10	45.5	33	2	US-08-343-443B-73	Sequence 73, Appl	C 626	10	45.5	47	1	US-08-340-820-26	Sequence 26, Appl
C 554	10	45.5	33	2	US-08-343-443B-93	Sequence 93, Appl	627	10	45.5	47	1	US-08-172-328-10	Sequence 10, Appl
C 555	10	45.5	34	1	US-07-825-959-8	Sequence 8, Appl1	C 628	10	45.5	47	1	US-08-172-328-10	Sequence 10, Appl
C 556	10	45.5	34	1	US-07-825-959-8	Sequence 8, Appl1	629	10	45.5	47	1	US-08-172-328-10	Sequence 10, Appl
C 557	10	45.5	34	1	US-08-131-324-8	Sequence 8, Appl1	C 630	10	45.5	48	1	US-08-593-535-26	Sequence 26, Appl
C 558	10	45.5	34	1	US-08-131-324-8	Sequence 8, Appl1	631	10	45.5	48	1	US-08-593-535-26	Sequence 26, Appl
C 559	10	45.5	34	1	US-08-647-584-6	Sequence 6, Appl1	C 632	10	45.5	48	1	US-08-389-459A-14	Sequence 14, Appl
C 560	10	45.5	34	1	US-08-647-584-6	Sequence 6, Appl1	633	10	45.5	48	3	US-08-389-459A-14	Sequence 14, Appl
C 561	10	45.5	34	4	US-09-358-972-255	Sequence 255, App	C 634	10	45.5	48	3	US-08-987-867A-14	Sequence 14, Appl
C 562	10	45.5	34	4	US-09-358-972-255	Sequence 255, App	635	10	45.5	49	4	US-09-363-970-27	Sequence 27, Appl
C 563	10	45.5	34	4	US-09-406-064-48	Sequence 48, Appl	C 636	10	45.5	49	4	US-09-363-970-27	Sequence 27, Appl
C 564	10	45.5	34	4	US-09-406-064-48	Sequence 48, Appl	637	9.8	44.5	18	1	US-08-334-847-895	Sequence 895, App
C 565	10	45.5	34	4	US-09-383-316-95	Sequence 95, Appl	C 638	9.8	44.5	18	1	US-08-334-847-895	Sequence 895, App
C 566	10	45.5	34	4	US-09-383-316-95	Sequence 95, Appl	639	9.8	44.5	20	1	US-08-031-147A-14	Sequence 14, Appl
C 567	10	45.5	35	4	US-08-235-836C-25	Sequence 25, Appl	C 640	9.8	44.5	20	1	US-08-031-147A-14	Sequence 14, Appl
C 568	10	45.5	35	4	US-08-235-836C-25	Sequence 25, Appl	641	9.8	44.5	20	1	US-07-872-678A-20	Sequence 20, Appl
C 569	10	45.5	36	1	US-08-122-321A-3	Sequence 3, Appl1	C 642	9.8	44.5	20	1	US-07-872-678A-20	Sequence 20, Appl
C 570	10	45.5	36	1	US-08-122-321A-3	Sequence 3, Appl1	643	9.8	44.5	20	1	US-08-512-681-24	Sequence 24, Appl
C 571	10	45.5	36	1	US-07-941-523-16	Sequence 16, Appl	C 644	9.8	44.5	20	1	US-08-512-681-24	Sequence 24, Appl
C 572	10	45.5	36	1	US-07-941-523-16	Sequence 16, Appl	645	9.8	44.5	20	2	US-08-403-888A-130	Sequence 130, App
C 573	10	45.5	36	1	US-08-368-803-21	Sequence 21, Appl	C 646	9.8	44.5	20	2	US-08-403-888A-130	Sequence 130, App
C 574	10	45.5	36	1	US-08-368-803-21	Sequence 21, Appl	647	9.8	44.5	20	4	US-09-103-875-110	Sequence 110, App
C 575	10	45.5	36	2	US-08-578-096A-22	Sequence 22, Appl	C 648	9.8	44.5	20	4	US-09-103-875-110	Sequence 110, App
C 576	10	45.5	36	2	US-08-578-096A-22	Sequence 22, Appl	649	9.8	44.5	20	4	US-09-560-594-33	Sequence 33, Appl
C 577	10	45.5	36	2	US-08-881-772-3	Sequence 3, Appl1	C 650	9.8	44.5	20	4	US-09-560-594-33	Sequence 33, Appl
C 578	10	45.5	36	3	US-08-881-772-3	Sequence 3, Appl1	651	9.8	44.5	20	5	PCT-US94-02471-14	Sequence 14, Appl
C 579	10	45.5	36	3	US-08-790-517-12	Sequence 12, Appl	C 652	9.8	44.5	20	5	PCT-US94-02471-14	Sequence 14, Appl
C 580	10	45.5	36	3	US-08-790-517-12	Sequence 12, Appl	653	9.8	44.5	21	4	US-08-406-030A-2	Sequence 2, Appl1
C 581	10	45.5	36	3	US-09-240-426-22	Sequence 22, Appl	C 654	9.8	44.5	21	4	US-08-406-030A-2	Sequence 2, Appl1
C 582	10	45.5	36	3	US-09-240-426-22	Sequence 22, Appl	655	9.8	44.5	22	4	US-09-347-114A-54	Sequence 54, Appl
C 583	10	45.5	36	3	US-09-219-932-18	Sequence 18, Appl	C 656	9.8	44.5	22	4	US-09-347-114A-54	Sequence 54, Appl
C 584	10	45.5	36	3	US-09-219-932-18	Sequence 18, Appl	657	9.8	44.5	23	2	US-08-403-853-23	Sequence 23, Appl
C 585	10	45.5	36	4	US-09-362-831-22	Sequence 22, Appl	C 658	9.8	44.5	23	2	US-08-403-853-23	Sequence 23, Appl
C 586	10	45.5	36	4	US-09-362-831-22	Sequence 22, Appl	659	9.8	44.5	23	4	US-09-182-117-7	Sequence 7, Appl1
C 587	10	45.5	36	5	PCT-US94-10130-3	Sequence 3, Appl1	C 660	9.8	44.5	23	4	US-09-182-117-7	Sequence 7, Appl1
C 588	10	45.5	37	1	PCT-US94-10130-3	Sequence 3, Appl1	661	9.8	44.5	23	4	US-08-482-918-90	Sequence 90, Appl
C 589	10	45.5	37	1	US-08-459-519-1	Sequence 1, Appl1	C 662	9.8	44.5	23	4	US-08-482-918-90	Sequence 90, Appl
C 590	10	45.5	37	1	US-08-459-519-1	Sequence 1, Appl1	663	9.8	44.5	23	4	US-09-224-681-90	Sequence 90, Appl
C 591	10	45.5	37	4	US-09-358-036-55	Sequence 55, Appl	C 664	9.8	44.5	23	4	US-09-224-681-90	Sequence 90, Appl
C 592	10	45.5	37	4	US-09-358-036-55	Sequence 55, Appl	665	9.8	44.5	23	4	US-08-336-728A-90	Sequence 90, Appl
C 593	10	45.5	38	1	US-08-117-907-10	Sequence 10, Appl	C 666	9.8	44.5	23	4	US-08-336-728A-90	Sequence 90, Appl
C 594	10	45.5	38	1	US-08-117-907-10	Sequence 10, Appl	667	9.8	44.5	24	2	US-08-353-476-49	Sequence 49, Appl
C 595	10	45.5	38	3	US-08-453-040-10	Sequence 10, Appl	C 668	9.8	44.5	24	2	US-08-353-476-49	Sequence 49, Appl
C 596	10	45.5	38	3	US-08-453-040-10	Sequence 10, Appl	669	9.8	44.5	24	2	US-08-353-476-49	Sequence 49, Appl
C 597	10	45.5	38	6	5281520-25	Patent No. 5281520	C 670	9.8	44.5	24	4	US-09-347-114A-23	Sequence 23, Appl
C 598	10	45.5	38	6	5281520-25	Patent No. 5281520	671	9.8	44.5	24	4	US-09-347-114A-23	Sequence 23, Appl
C 599	10	45.5	39	1	US-08-197-770-16	Sequence 16, Appl	C 672	9.8	44.5	25	3	US-08-513-974B-13	Sequence 13, Appl
C 600	10	45.5	39	1	US-08-197-770-16	Sequence 16, Appl	673	9.8	44.5	25	3	US-08-513-974B-13	Sequence 13, Appl
C 601	10	45.5	39	4	US-08-973-124-303	Sequence 303, App	C 674	9.8	44.5	25	3	US-08-513-974B-13	Sequence 13, Appl
C 602	10	45.5	39	4	US-08-973-124-303	Sequence 303, App	675	9.8	44.5	26	2	US-08-859-998-860	Sequence 860, App
C 603	10	45.5	39	5	PCT-US96-08014-303	Sequence 303, App	C 676	9.8	44.5	26	2	US-08-859-998-860	Sequence 860, App
C 604	10	45.5	39	5	PCT-US96-08014-303	Sequence 303, App	677	9.8	44.5	26	4	US-09-347-114A-39	Sequence 39, Appl
C 605	10	45.5	39	6	5223482-34	Patent No. 5223482	C 678	9.8	44.5	26	4	US-09-347-114A-39	Sequence 39, Appl
C 606	10	45.5	39	6	5223482-34	Patent No. 5223482	679	9.8	44.5	26	4	US-09-325-928-860	Sequence 860, App
C 607	10	45.5	40	4	US-09-383-143-39	Sequence 39, Appl	C 680	9.8	44.5	26	4	US-09-325-928-860	Sequence 860, App
C 608	10	45.5	40	4	US-09-383-143-39	Sequence 39, Appl	681	9.8	44.5	26	5	PCT-US92-0809A-34	Sequence 34, Appl
C 609	10	45.5	41	1	US-08-340-820-27	Sequence 27, Appl	C 682	9.8	44.5	26	5	PCT-US92-0809A-34	Sequence 34, Appl
C 610	10	45.5	41	1	US-08-340-820-27	Sequence 27, Appl	683	9.8	44.5	27	2	US-08-951-718-2	Sequence 2, Appl1
C 611	10	45.5	41	1	US-08-172-328-11	Sequence 11, Appl	C 684	9.8	44.5	27	2	US-08-951-718-2	Sequence 2, Appl1

685	9.8	44.5	27	3	US-09-126-280-17	Sequence 17, Appl	758	9.8	44.5	36	3	US-09-213-053-12	Sequence 12, Appl
C 686	9.8	44.5	27	3	US-09-126-280-17	Sequence 17, Appl	759	9.8	44.5	36	3	US-09-213-053-13	Sequence 13, Appl
C 687	9.8	44.5	27	4	US-08-584-040-5232	Sequence 5232, Ap	C 760	9.8	44.5	36	3	US-09-213-053-16	Sequence 16, Appl
C 688	9.8	44.5	28	4	US-08-584-040-5232	Sequence 5232, Ap	C 761	9.8	44.5	36	3	US-09-213-053-16	Sequence 16, Appl
C 689	9.8	44.5	28	4	US-09-347-114A-45	Sequence 45, Appl	C 762	9.8	44.5	36	3	US-09-213-053-17	Sequence 17, Appl
C 690	9.8	44.5	28	4	US-09-347-114A-45	Sequence 45, Appl	C 763	9.8	44.5	36	3	US-09-213-053-17	Sequence 17, Appl
C 691	9.8	44.5	29	1	US-08-233-788A-27	Sequence 27, Appl	C 764	9.8	44.5	37	2	US-08-874-678-14	Sequence 14, Appl
C 692	9.8	44.5	29	1	US-08-233-788A-27	Sequence 27, Appl	C 765	9.8	44.5	37	2	US-08-874-678-14	Sequence 14, Appl
C 693	9.8	44.5	30	1	US-08-450-945-29	Sequence 29, Appl	C 766	9.8	44.5	37	2	US-08-874-678-14	Sequence 14, Appl
C 694	9.8	44.5	30	1	US-08-450-945-29	Sequence 29, Appl	C 767	9.8	44.5	37	3	US-08-643-839-14	Sequence 14, Appl
C 695	9.8	44.5	30	2	US-08-174-672D-73	Sequence 73, Appl	C 768	9.8	44.5	37	3	US-08-643-839-14	Sequence 14, Appl
C 696	9.8	44.5	30	2	US-08-174-672D-73	Sequence 73, Appl	C 769	9.8	44.5	37	4	US-09-348-886-14	Sequence 14, Appl
C 697	9.8	44.5	30	3	US-07-705-490-10	Sequence 10, Appl	C 770	9.8	44.5	37	4	US-09-348-886-14	Sequence 14, Appl
C 698	9.8	44.5	30	3	US-07-705-490-10	Sequence 10, Appl	C 771	9.8	44.5	38	3	US-08-724-752-8	Sequence 8, Appl
C 699	9.8	44.5	30	3	US-08-758-662-6	Sequence 6, Appl	C 772	9.8	44.5	38	3	US-08-724-752-8	Sequence 8, Appl
C 700	9.8	44.5	30	3	US-08-758-662-6	Sequence 6, Appl	C 773	9.8	44.5	38	3	US-09-213-053-20	Sequence 20, Appl
C 701	9.8	44.5	30	4	US-07-751-891B-10	Sequence 10, Appl	C 774	9.8	44.5	38	3	US-09-213-053-20	Sequence 20, Appl
C 702	9.8	44.5	30	4	US-07-751-891B-10	Sequence 10, Appl	C 775	9.8	44.5	39	4	US-09-262-773-101	Sequence 101, Appl
C 703	9.8	44.5	30	4	US-07-751-891B-10	Sequence 10, Appl	C 776	9.8	44.5	39	4	US-09-262-773-101	Sequence 101, Appl
C 704	9.8	44.5	30	4	US-07-751-891B-16	Sequence 16, Appl	C 777	9.8	44.5	40	1	US-08-032-846-35	Sequence 35, Appl
C 705	9.8	44.5	30	4	US-08-976-161-29	Sequence 29, Appl	C 778	9.8	44.5	40	1	US-08-032-846-35	Sequence 35, Appl
C 706	9.8	44.5	30	4	US-08-976-161-29	Sequence 29, Appl	C 779	9.8	44.5	40	1	US-08-474-636-35	Sequence 35, Appl
C 707	9.8	44.5	31	2	US-08-956-047-4	Sequence 4, Appl	C 780	9.8	44.5	40	4	US-08-474-636-35	Sequence 35, Appl
C 708	9.8	44.5	31	2	US-08-956-047-4	Sequence 4, Appl	C 781	9.8	44.5	41	1	US-08-530-492-79	Sequence 79, Appl
C 709	9.8	44.5	31	2	US-08-924-695A-9	Sequence 9, Appl	C 782	9.8	44.5	41	1	US-08-530-492-79	Sequence 79, Appl
C 710	9.8	44.5	31	2	US-08-924-695A-9	Sequence 9, Appl	C 783	9.8	44.5	41	4	US-08-906-517-79	Sequence 79, Appl
C 711	9.8	44.5	31	3	US-08-504-878A-3	Sequence 3, Appl	C 784	9.8	44.5	41	4	US-08-906-517-79	Sequence 79, Appl
C 712	9.8	44.5	31	3	US-08-504-878A-3	Sequence 3, Appl	C 785	9.8	44.5	41	4	US-09-293-569-5	Sequence 5, Appl
C 713	9.8	44.5	31	4	US-09-246-277A-9	Sequence 9, Appl	C 786	9.8	44.5	41	4	US-09-293-569-5	Sequence 5, Appl
C 714	9.8	44.5	31	4	US-09-246-277A-9	Sequence 9, Appl	C 787	9.8	44.5	41	4	US-09-363-970-13	Sequence 13, Appl
C 715	9.8	44.5	32	1	US-08-181-556-4	Sequence 4, Appl	C 788	9.8	44.5	42	1	US-09-363-970-13	Sequence 13, Appl
C 716	9.8	44.5	32	1	US-08-181-556-4	Sequence 4, Appl	C 789	9.8	44.5	42	1	US-08-530-492-145	Sequence 145, Appl
C 717	9.8	44.5	32	2	US-08-697-631A-1	Sequence 1, Appl	C 790	9.8	44.5	42	1	US-08-530-492-145	Sequence 145, Appl
C 718	9.8	44.5	32	2	US-08-697-631A-1	Sequence 1, Appl	C 791	9.8	44.5	42	1	US-08-466-033-156	Sequence 156, Appl
C 719	9.8	44.5	33	1	US-08-276-852-163	Sequence 163, App	C 792	9.8	44.5	42	1	US-08-466-033-156	Sequence 156, Appl
C 720	9.8	44.5	33	1	US-08-276-852-163	Sequence 163, App	C 793	9.8	44.5	42	1	US-08-444-733-156	Sequence 156, Appl
C 721	9.8	44.5	33	1	US-08-276-852-166	Sequence 166, App	C 794	9.8	44.5	42	1	US-08-444-733-156	Sequence 156, Appl
C 722	9.8	44.5	33	1	US-08-276-852-166	Sequence 166, App	C 795	9.8	44.5	42	2	US-08-464-134-156	Sequence 156, App
C 723	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 796	9.8	44.5	42	2	US-08-464-134-156	Sequence 156, App
C 724	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 797	9.8	44.5	42	2	US-08-461-361-156	Sequence 156, App
C 725	9.8	44.5	33	1	US-08-899-575-166	Sequence 166, App	C 798	9.8	44.5	42	2	US-08-461-361-156	Sequence 156, App
C 726	9.8	44.5	33	1	US-08-899-575-166	Sequence 166, App	C 799	9.8	44.5	42	2	US-08-485-910-156	Sequence 156, App
C 727	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 800	9.8	44.5	42	2	US-08-485-910-156	Sequence 156, App
C 728	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 801	9.8	44.5	42	4	US-08-906-517-145	Sequence 145, App
C 729	9.8	44.5	33	1	US-08-899-575-166	Sequence 166, App	C 802	9.8	44.5	42	4	US-08-906-517-145	Sequence 145, App
C 730	9.8	44.5	33	3	US-08-819-177-29	Sequence 29, Appl	C 803	9.8	44.5	45	1	US-08-554-133-2	Sequence 2, Appl
C 731	9.8	44.5	33	3	US-08-819-177-29	Sequence 29, Appl	C 804	9.8	44.5	45	1	US-08-554-133-2	Sequence 2, Appl
C 732	9.8	44.5	33	4	US-08-943-136-14	Sequence 14, Appl	C 805	9.8	44.5	49	4	US-09-538-709-122	Sequence 122, App
C 733	9.8	44.5	33	4	US-08-943-136-14	Sequence 14, Appl	C 806	9.8	44.5	49	4	US-09-538-709-122	Sequence 122, App
C 734	9.8	44.5	33	4	US-08-943-136-14	Sequence 14, Appl	C 807	9.8	44.5	49	4	US-09-538-709-1285	Sequence 1285, Ap
C 735	9.8	44.5	33	4	US-08-973-518-14	Sequence 14, Appl	C 808	9.8	44.5	50	1	US-07-977-696C-55	Sequence 55, Appl
C 736	9.8	44.5	33	4	US-08-973-518-14	Sequence 14, Appl	C 809	9.8	44.5	50	1	US-07-977-696C-55	Sequence 55, Appl
C 737	9.8	44.5	33	5	PCT-US95-08743-163	Sequence 163, App	C 810	9.8	44.5	50	1	US-07-977-696C-55	Sequence 55, Appl
C 738	9.8	44.5	33	5	PCT-US95-08743-163	Sequence 163, App	C 811	9.8	44.5	50	1	US-08-129-930B-55	Sequence 55, Appl
C 739	9.8	44.5	33	5	PCT-US95-08743-166	Sequence 166, App	C 812	9.8	44.5	50	1	US-08-129-930B-55	Sequence 55, Appl
C 740	9.8	44.5	33	5	PCT-US95-08743-166	Sequence 166, App	C 813	9.8	44.5	50	4	US-08-976-288A-55	Sequence 55, Appl
C 741	9.8	44.5	35	1	US-08-451-240-39	Sequence 39, Appl	C 814	9.8	44.5	50	4	US-08-976-288A-55	Sequence 55, Appl
C 742	9.8	44.5	35	1	US-08-451-240-39	Sequence 39, Appl	C 815	9.8	44.5	19	4	US-09-305-927-33	Sequence 33, Appl
C 743	9.8	44.5	35	1	US-08-664-449-20	Sequence 20, Appl	C 816	9.8	44.5	19	4	US-09-305-927-33	Sequence 33, Appl
C 744	9.8	44.5	35	1	US-08-664-449-20	Sequence 20, Appl	C 817	9.8	44.5	20	1	US-08-460-130-1	Sequence 1, Appl
C 745	9.8	44.5	35	2	US-08-470-846A-35	Sequence 35, Appl	C 818	9.8	44.5	20	1	US-08-460-130-1	Sequence 1, Appl
C 746	9.8	44.5	35	2	US-08-470-846A-35	Sequence 35, Appl	C 819	9.8	44.5	20	1	US-08-484-607A-56	Sequence 56, Appl
C 747	9.8	44.5	35	3	US-08-967-272-5	Sequence 5, Appl	C 820	9.8	44.5	20	1	US-08-484-607A-56	Sequence 56, Appl
C 748	9.8	44.5	35	3	US-08-967-272-5	Sequence 5, Appl	C 821	9.8	44.5	20	1	US-08-557-139-30	Sequence 30, Appl
C 749	9.8	44.5	35	5	PCT-US94-12591-39	Sequence 39, Appl	C 822	9.8	44.5	20	1	US-08-557-139-30	Sequence 30, Appl
C 750	9.8	44.5	35	5	PCT-US94-12591-39	Sequence 39, Appl	C 823	9.8	44.5	20	3	US-08-962-169-56	Sequence 56, Appl
C 751	9.8	44.5	36	1	US-08-291-932A-445	Sequence 445, App	C 824	9.8	44.5	20	3	US-08-962-169-56	Sequence 56, Appl
C 752	9.8	44.5	36	1	US-08-291-932A-445	Sequence 445, App	C 825	9.8	44.5	20	4	US-09-487-368A-129	Sequence 129, App
C 753	9.8	44.5	36	1	US-08-363-240A-914	Sequence 914, App	C 826	9.8	44.5	22	6	5202236-29	Patent No. 5202236
C 754	9.8	44.5	36	1	US-08-363-240A-914	Sequence 914, App	C 827	9.8	44.5	22	6	5202236-29	Patent No. 5202236
C 755	9.8	44.5	36	1	US-08-311-486C-855	Sequence 855, App	C 828	9.8	44.5	23	2	US-08-859-998-816	Sequence 816, App
C 756	9.8	44.5	36	1	US-08-311-486C-855	Sequence 855, App	C 829	9.8	44.5	23	2	US-08-859-998-816	Sequence 816, App
C 757	9.8	44.5	36	3	US-09-213-053-12	Sequence 12, Appl	C 830	9.8	44.5	23	2	US-08-859-998-816	Sequence 816, App

C 831	9.6	43.6	23	4	US-09-225-928-816	Sequence 816, App	C 904	9.6	43.6	36	4	US-08-848-760B-18	Sequence 18, Appl
C 832	9.6	43.6	23	4	US-09-225-928-816	Sequence 816, App	C 905	9.6	43.6	36	4	US-09-374-962-17	Sequence 17, Appl
C 833	9.6	43.6	23	4	US-09-122-126B-10	Sequence 10, Appl	C 906	9.6	43.6	36	4	US-09-374-962-17	Sequence 17, Appl
C 834	9.6	43.6	23	4	US-09-122-126B-10	Sequence 10, Appl	C 907	9.6	43.6	38	1	US-08-390-850-857	Sequence 857, App
C 835	9.6	43.6	24	1	US-08-460-344-38	Sequence 38, Appl	C 908	9.6	43.6	38	1	US-08-390-850-857	Sequence 857, App
C 836	9.6	43.6	24	1	US-08-460-344-38	Sequence 38, Appl	C 909	9.6	43.6	38	1	US-08-390-850-923	Sequence 923, App
C 837	9.6	43.6	24	1	US-08-460-344-62	Sequence 62, Appl	C 910	9.6	43.6	38	1	US-08-390-850-923	Sequence 923, App
C 838	9.6	43.6	24	1	US-08-460-344-62	Sequence 62, Appl	C 911	9.6	43.6	38	1	US-08-390-850-923	Sequence 923, App
C 839	9.6	43.6	24	1	US-08-133-598A-38	Sequence 38, Appl	C 912	9.6	43.6	38	1	US-08-390-850-923	Sequence 923, App
C 840	9.6	43.6	24	1	US-08-133-598A-38	Sequence 38, Appl	C 913	9.6	43.6	38	1	US-08-390-850-923	Sequence 923, App
C 841	9.6	43.6	24	1	US-08-133-598A-62	Sequence 62, Appl	C 914	9.6	43.6	38	1	US-08-373-124A-259	Sequence 259, App
C 842	9.6	43.6	24	1	US-08-133-598A-62	Sequence 62, Appl	C 915	9.6	43.6	38	1	US-08-373-124A-1346	Sequence 1346, App
C 843	9.6	43.6	24	1	US-08-558-420-3	Sequence 3, Appl	C 916	9.6	43.6	38	1	US-08-373-124A-1346	Sequence 1346, App
C 844	9.6	43.6	24	1	US-08-558-420-3	Sequence 3, Appl	C 917	9.6	43.6	38	1	US-08-373-124A-1750	Sequence 1750, App
C 845	9.6	43.6	24	1	US-08-886-999-38	Sequence 38, Appl	C 918	9.6	43.6	38	1	US-08-373-124A-1750	Sequence 1750, App
C 846	9.6	43.6	24	1	US-08-886-999-38	Sequence 38, Appl	C 919	9.6	43.6	38	1	US-08-373-124A-1936	Sequence 1936, App
C 847	9.6	43.6	24	1	US-08-886-999-62	Sequence 62, Appl	C 920	9.6	43.6	38	1	US-08-373-124A-1936	Sequence 1936, App
C 848	9.6	43.6	24	1	US-08-886-999-62	Sequence 62, Appl	C 921	9.6	43.6	38	1	US-08-373-124A-2292	Sequence 2292, App
C 849	9.6	43.6	24	2	US-08-353-476-51	Sequence 51, Appl	C 922	9.6	43.6	38	1	US-08-373-124A-2292	Sequence 2292, App
C 850	9.6	43.6	24	2	US-08-353-476-51	Sequence 51, Appl	C 923	9.6	43.6	38	1	US-08-373-124A-2428	Sequence 2428, App
C 851	9.6	43.6	24	5	PCT-US93-05085-39	Sequence 39, Appl	C 924	9.6	43.6	38	1	US-08-373-124A-2428	Sequence 2428, App
C 852	9.6	43.6	24	5	PCT-US93-05085-39	Sequence 39, Appl	C 925	9.6	43.6	38	1	US-08-373-124A-2476	Sequence 2476, App
C 853	9.6	43.6	25	2	US-08-590-674-1	Sequence 1, Appl	C 926	9.6	43.6	38	1	US-08-373-124A-2476	Sequence 2476, App
C 854	9.6	43.6	25	2	US-08-590-674-1	Sequence 1, Appl	C 927	9.6	43.6	38	1	US-08-335-634-857	Sequence 857, App
C 855	9.6	43.6	25	2	US-08-590-674-1	Sequence 1, Appl	C 928	9.6	43.6	38	1	US-08-335-634-857	Sequence 857, App
C 856	9.6	43.6	25	4	US-09-315-793-19	Sequence 19, Appl	C 929	9.6	43.6	38	1	US-08-435-634-923	Sequence 923, App
C 857	9.6	43.6	25	4	US-09-315-793-19	Sequence 19, Appl	C 930	9.6	43.6	38	1	US-08-435-634-923	Sequence 923, App
C 858	9.6	43.6	25	4	US-09-395-345-34	Sequence 34, Appl	C 931	9.6	43.6	38	1	US-08-435-634-931	Sequence 931, App
C 859	9.6	43.6	26	1	US-08-664-449-21	Sequence 21, Appl	C 932	9.6	43.6	38	1	US-08-435-634-931	Sequence 931, App
C 860	9.6	43.6	26	1	US-08-664-449-21	Sequence 21, Appl	C 933	9.6	43.6	38	1	US-08-435-628-259	Sequence 259, App
C 861	9.6	43.6	28	3	US-08-474-700B-6	Sequence 6, Appl	C 934	9.6	43.6	38	1	US-08-435-628-259	Sequence 259, App
C 862	9.6	43.6	28	3	US-08-474-700B-6	Sequence 6, Appl	C 935	9.6	43.6	38	1	US-08-435-628-1346	Sequence 1346, App
C 863	9.6	43.6	28	4	US-09-338-420-6	Sequence 6, Appl	C 936	9.6	43.6	38	1	US-08-435-628-1346	Sequence 1346, App
C 864	9.6	43.6	28	4	US-09-338-420-6	Sequence 6, Appl	C 937	9.6	43.6	38	1	US-08-435-628-1750	Sequence 1750, App
C 865	9.6	43.6	28	5	PCT-US95-05812-6	Sequence 6, Appl	C 938	9.6	43.6	38	1	US-08-435-628-1750	Sequence 1750, App
C 866	9.6	43.6	29	5	PCT-US95-05812-6	Sequence 6, Appl	C 939	9.6	43.6	38	1	US-08-435-628-1936	Sequence 1936, App
C 867	9.6	43.6	29	4	US-08-843-572E-7	Sequence 7, Appl	C 940	9.6	43.6	38	1	US-08-435-628-1936	Sequence 1936, App
C 868	9.6	43.6	29	4	US-08-843-572E-7	Sequence 7, Appl	C 941	9.6	43.6	38	1	US-08-435-628-2292	Sequence 2292, App
C 869	9.6	43.6	30	2	US-08-353-372A-31	Sequence 31, Appl	C 942	9.6	43.6	38	1	US-08-435-628-2292	Sequence 2292, App
C 870	9.6	43.6	30	2	US-08-353-372A-31	Sequence 31, Appl	C 943	9.6	43.6	38	1	US-08-435-628-2428	Sequence 2428, App
C 871	9.6	43.6	30	3	US-08-462-436-4	Sequence 4, Appl	C 944	9.6	43.6	38	1	US-08-435-628-2428	Sequence 2428, App
C 872	9.6	43.6	30	3	US-08-462-436-4	Sequence 4, Appl	C 945	9.6	43.6	38	1	US-08-435-628-2476	Sequence 2476, App
C 873	9.6	43.6	30	3	US-08-465-275-4	Sequence 4, Appl	C 946	9.6	43.6	38	1	US-08-435-628-2476	Sequence 2476, App
C 874	9.6	43.6	30	3	US-08-465-275-4	Sequence 4, Appl	C 947	9.6	43.6	38	2	US-08-292-620A-2162	Sequence 2162, App
C 875	9.6	43.6	30	4	US-09-493-352A-6	Sequence 6, Appl	C 948	9.6	43.6	38	2	US-08-292-620A-2162	Sequence 2162, App
C 876	9.6	43.6	30	4	US-09-493-352A-6	Sequence 6, Appl	C 949	9.6	43.6	38	3	US-09-071-845-2162	Sequence 2162, App
C 877	9.6	43.6	30	4	US-08-057-430A-22	Sequence 22, Appl	C 950	9.6	43.6	38	3	US-09-071-845-2162	Sequence 2162, App
C 878	9.6	43.6	30	4	US-08-057-430A-22	Sequence 22, Appl	C 951	9.6	43.6	39	1	US-08-527-734-19	Sequence 19, Appl
C 879	9.6	43.6	30	4	US-08-640-877-4	Sequence 4, Appl	C 952	9.6	43.6	39	1	US-08-527-734-19	Sequence 19, Appl
C 880	9.6	43.6	30	4	US-08-640-877-4	Sequence 4, Appl	C 953	9.6	43.6	39	1	US-08-527-734-20	Sequence 20, Appl
C 881	9.6	43.6	31	4	US-08-679-645-497	Sequence 497, App	C 954	9.6	43.6	39	1	US-08-527-734-20	Sequence 20, Appl
C 882	9.6	43.6	31	4	US-08-679-645-497	Sequence 497, App	C 955	9.6	43.6	39	4	US-08-592-459-9	Sequence 9, Appl
C 883	9.6	43.6	33	1	US-08-664-449-22	Sequence 22, Appl	C 956	9.6	43.6	39	4	US-08-592-459-9	Sequence 9, Appl
C 884	9.6	43.6	33	1	US-08-664-449-22	Sequence 22, Appl	C 957	9.6	43.6	39	5	PCT-US91-08525-9	Sequence 9, Appl
C 885	9.6	43.6	33	4	US-09-257-580-6	Sequence 6, Appl	C 958	9.6	43.6	39	5	PCT-US91-08525-9	Sequence 9, Appl
C 886	9.6	43.6	33	4	US-09-257-580-6	Sequence 6, Appl	C 959	9.6	43.6	39	5	PCT-US93-04384-33	Sequence 33, Appl
C 887	9.6	43.6	34	3	US-08-951-923-54	Sequence 54, Appl	C 960	9.6	43.6	39	5	PCT-US93-04384-33	Sequence 33, Appl
C 888	9.6	43.6	34	3	US-08-951-923-54	Sequence 54, Appl	C 961	9.6	43.6	40	4	US-09-485-737B-9	Sequence 9, Appl
C 889	9.6	43.6	34	3	US-08-961-083-452	Sequence 452, App	C 962	9.6	43.6	40	4	US-09-485-737B-9	Sequence 9, Appl
C 890	9.6	43.6	34	3	US-08-961-083-452	Sequence 452, App	C 963	9.6	43.6	42	1	US-08-401-908-25	Sequence 25, Appl
C 891	9.6	43.6	35	2	US-08-458-970A-4	Sequence 4, Appl	C 964	9.6	43.6	42	1	US-08-401-908-25	Sequence 25, Appl
C 892	9.6	43.6	35	2	US-08-458-970A-4	Sequence 4, Appl	C 965	9.6	43.6	44	1	US-07-991-587A-4	Sequence 4, Appl
C 893	9.6	43.6	35	4	US-09-374-962-18	Sequence 18, Appl	C 966	9.6	43.6	44	1	US-07-991-587A-4	Sequence 4, Appl
C 894	9.6	43.6	35	4	US-09-374-962-18	Sequence 18, Appl	C 967	9.6	43.6	44	1	US-08-309-985-4	Sequence 4, Appl
C 895	9.6	43.6	36	1	US-08-644-664B-2	Sequence 2, Appl	C 968	9.6	43.6	44	1	US-08-309-985-4	Sequence 4, Appl
C 896	9.6	43.6	36	1	US-08-644-664B-2	Sequence 2, Appl	C 969	9.6	43.6	44	1	US-08-105-483-41	Sequence 41, Appl
C 897	9.6	43.6	36	2	US-08-761-277A-2	Sequence 2, Appl	C 970	9.6	43.6	44	1	US-08-105-483-41	Sequence 41, Appl
C 898	9.6	43.6	36	2	US-08-761-277A-2	Sequence 2, Appl	C 971	9.6	43.6	44	1	US-08-073-962-41	Sequence 41, Appl
C 899	9.6	43.6	36	4	US-08-821-278A-5	Sequence 5, Appl	C 972	9.6	43.6	44	1	US-08-073-962-41	Sequence 41, Appl
C 900	9.6	43.6	36	4	US-08-821-278A-5	Sequence 5, Appl	C 973	9.6	43.6	44	1	US-07-714-687-53	Sequence 53, Appl
C 901	9.6	43.6	36	4	US-08-821-278A-9	Sequence 9, Appl	C 974	9.6	43.6	44	1	US-07-714-687-53	Sequence 53, Appl
C 902	9.6	43.6	36	4	US-08-821-278A-9	Sequence 9, Appl	C 975	9.6	43.6	44	1	US-08-224-391-92	Sequence 92, Appl
C 903	9.6	43.6	36	4	US-08-848-760B-18	Sequence 18, Appl	C 976	9.6	43.6	44	1	US-08-224-391-92	Sequence 92, Appl

977 9.6 43.6 44 1 US-08-484-304-92 Sequence 92, Appl
c 978 9.6 43.6 44 1 US-08-484-304-92 Sequence 92, Appl
979 9.6 43.6 44 1 US-08-487-412-41 Sequence 41, Appl
c 980 9.6 43.6 44 1 US-08-487-412-41 Sequence 41, Appl
981 9.6 43.6 44 1 US-08-709-209-41 Sequence 41, Appl
c 982 9.6 43.6 44 1 US-08-709-209-41 Sequence 41, Appl
983 9.6 43.6 44 1 US-08-458-101-41 Sequence 41, Appl
c 984 9.6 43.6 44 1 US-08-458-101-41 Sequence 41, Appl
985 9.4 42.7 17 2 US-08-970-269A-14 Sequence 14, Appl
c 986 9.4 42.7 17 2 US-08-970-269A-14 Sequence 14, Appl
987 9.4 42.7 17 4 US-09-407-562-14 Sequence 14, Appl
c 988 9.4 42.7 17 4 US-09-407-562-14 Sequence 14, Appl
989 9.4 42.7 17 4 US-09-375-318-49 Sequence 49, Appl
c 990 9.4 42.7 17 4 US-09-375-318-49 Sequence 49, Appl
991 9.4 42.7 18 4 US-09-122-400B-19 Sequence 19, Appl
c 992 9.4 42.7 18 4 US-09-122-400B-19 Sequence 19, Appl
993 9.4 42.7 20 1 US-08-356-405-11 Sequence 11, Appl
c 994 9.4 42.7 20 1 US-08-356-405-11 Sequence 11, Appl
995 9.4 42.7 20 2 US-08-910-629A-58 Sequence 58, Appl
c 996 9.4 42.7 20 2 US-08-910-629A-58 Sequence 58, Appl
997 9.4 42.7 20 2 US-09-289-368-52 Sequence 52, Appl
c 998 9.4 42.7 20 2 US-09-289-368-52 Sequence 52, Appl
999 9.4 42.7 20 3 US-08-888-998-7 Sequence 7, Appl
c1000 9.4 42.7 20 3 US-08-888-998-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-042-353-391

Sequence 391, Application US/09042353

Patent No. 6255458

GENERAL INFORMATION:

APPLICANT: Lonberg, Nile

TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for

TITLE OF INVENTION: Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 421

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042.353

FILING DATE: 13-MAR-1998

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/810,279

FILING DATE: 17-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/853,408

FILING DATE: 18-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/904,068

FILING DATE: 23-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,131

FILING DATE: 26-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/096,762

FILING DATE: 22-JUL-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643--009040US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 391:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-09-042-353-391

Query Match

Best Local Similarity 76.2%; Score 13; DB 4; Length 44;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGCCGATGATGCTCCAG 22
DB 9 TGAGAGTGAATCTGTCGAG 29

RESULT 2

US-09-042-353-391/c

Sequence 391, Application US/09042353

Patent No. 6255458

GENERAL INFORMATION:

APPLICANT: Lonberg, Nile

TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for

TITLE OF INVENTION: Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 421

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
APPLICATION NUMBER: US 07/810,279
PRIORITY INFORMATION DATA:
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
FILING DATE: 07/853,408
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 391:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-391

Query Match 59.1%; Score 13; DB 4; Length 44;

Best Local Similarity 76.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGAGCCGATATCGCTCTA 21
Db 29 CTGAGCAGATTTCACCTCA 9

RESULT 3
US-08-758-417A-241
Sequence 241, Application US/08/758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-758-417A-241

Query Match 59.1%; Score 13; DB 4; Length 44;

Best Local Similarity 76.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGTCTCAG 22
Db 9 TGAGAGTGAATCTGTCCAG 29

RESULT 4

US-08-758-417A-241/C
Sequence 241, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
KAY, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-758-417A-241

Query Match 59.1%; Score 13; DB 4; Length 44;

Best Local Similarity 76.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCA 21
Db 29 CTGAGACGATTTCACTCTCA 9

RESULT 5

US-08-235-503B-61
Sequence 61, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Baichwal, Vijay R
APPLICANT: Strulovici, Berta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-Apr-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-235-503B-61

Query Match 56.4%; Score 12.4; DB 1; Length 30;
Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 5 CTGTCACGAAACGCTACAG 26

RESULT 6

US-08-235-503B-61/C
Sequence 61, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Baichwal, Vijay R
APPLICANT: Strulovici, Berta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400


```

: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/235,503B
: FILING DATE: 29-APR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A
: REGISTRATION NUMBER: 36,627
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 398-3249
: TELEFAX: (415) 398-3249
: TELEX: 910 277299
: INFORMATION FOR SEQ ID NO: 61:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-235-503B-61

```

```

Query Match      56.4%; Score 12.4; DB 1; Length 30;
Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 1 CTGAGACCGATATCGCTCTAG 22
Db 26 CTGCTACCGTTTTCGTACACAG 5

```

```

RESULT 7
PCT-US95-05265-61
: Sequence 61, Application PC/TUS9505265
: GENERAL INFORMATION:
: APPLICANT: TULARIK, INC.
: TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
: NUMBER OF SEQUENCES: 74
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/05265
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/235,503
: FILING DATE: 29-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A
: REGISTRATION NUMBER: 36,627
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELEX: 910 277299

```

```

: INFORMATION FOR SEQ ID NO: 61:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: PCT-US95-05265-61

```

```

Query Match      56.4%; Score 12.4; DB 5; Length 30;
Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 CTGAGACCGATATCGCTCTAG 22
Db 5 CTGCTACCGAAACGCTACACAG 26

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RESULT 8
PCT-US95-05265-61/c
: Sequence 61, Application PC/TUS9505265
: GENERAL INFORMATION:
: APPLICANT: TULARIK, INC.
: TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
: NUMBER OF SEQUENCES: 74
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/05265
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/235,503
: FILING DATE: 29-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A
: REGISTRATION NUMBER: 36,627
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELEX: 910 277299
: INFORMATION FOR SEQ ID NO: 61:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: PCT-US95-05265-61

```

```

Query Match      56.4%; Score 12.4; DB 5; Length 30;
Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 1 CTGAGACCGATATCGCTCTAG 22
Db 26 CTGCTACCGTTTTCGTACACAG 5

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RESULT 9
US-08-956-047-22
: Sequence 22, Application US/08956047

```

Patent No. 5882924
GENERAL INFORMATION:
APPLICANT: Fritz, Hans-Joachim
APPLICANT: Hennecke, Frank
APPLICANT: Kolmar, Harald
TITLE OF INVENTION: Genetic Selection, by Means of Signal
TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are
TITLE OF INVENTION: Capable of Ligand Binding
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,047
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/257,669
FILING DATE: 08-JUN-1994
APPLICATION NUMBER: DE P 43 19 296.3
FILING DATE: 10-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pohlman, Sandra M.
REGISTRATION NUMBER: P39,691
REFERENCE/DOCKET NUMBER: 05552.1368-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-956-047-22

Query Match 56.4%; Score 12.4; DB 2; Length 32;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGATATCGCTCTCA 21
DB 9 CGATATCGCTCTCA 22

RESULT 10
US-08-956-047-22/C
Sequence 22, Application US/08956047
Patent No. 5882924
GENERAL INFORMATION:
APPLICANT: Fritz, Hans-Joachim
APPLICANT: Hennecke, Frank
APPLICANT: Kolmar, Harald
TITLE OF INVENTION: Genetic Selection, by Means of Signal
TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are
TITLE OF INVENTION: Capable of Ligand Binding
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 600
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,047
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/257,669
FILING DATE: 08-JUN-1994
APPLICATION NUMBER: DE P 43 19 296.3
FILING DATE: 10-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pohlman, Sandra M.
REGISTRATION NUMBER: P39,691
REFERENCE/DOCKET NUMBER: 05552.1368-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-956-047-22

Query Match 56.4%; Score 12.4; DB 2; Length 32;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCATATCG 15
DB 22 TGAGACCATATCG 9

RESULT 11
US-08-447-422-1
Sequence 1, Application US/08447422
Patent No. 5686579
GENERAL INFORMATION:
APPLICANT: SHAWI, Ezekiel Y.
APPLICANT: ROTHSTEIN, Aseer
APPLICANT: RAMJESINGH, Monabit
TITLE OF INVENTION: Use of Antibody/Antigen Interactions To
TITLE OF INVENTION: Protect or Modulate Biological Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,422
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,410
FILING DATE: 22-JUN-1993
APPLICATION NUMBER: US 07/938,505
FILING DATE: 31-AUG-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/205,748
; FILING DATE: 21-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17923/102 HYLI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 29
; OTHER INFORMATION: /mod_base= 1
;
US-08-447-422-1

Query Match      55.5%; Score 12.2; DB 1; Length 33;
Best Local Similarity 70.6%; Pred. No. 1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
Db      5 GACCGATATGCTCTBA 21

RESULT 12
US-08-447-422-1/c
; Sequence 1, Application US/08447422
; Patent No. 5686579
; GENERAL INFORMATION:
; APPLICANT: SHAMI, Ezekiel Y.
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: RAMJESINGH, Mohabir
; TITLE OF INVENTION: Use of Antibody/Antigen Interactions To
; TITLE OF INVENTION: Protect or Modulate Biological Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,422
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,410
; FILING DATE: 22-JUN-1993
; APPLICATION NUMBER: US 07/938,505
; FILING DATE: 31-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/205,748
; FILING DATE: 21-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17923/102 HYLI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
```

```
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 29
; OTHER INFORMATION: /mod_base= 1
;
US-08-447-422-1

Query Match      55.5%; Score 12.2; DB 1; Length 33;
Best Local Similarity 70.6%; Pred. No. 1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGAGACCGATATCGCTC 18
Db      21 TVAGSACRATRTCGCTC 5

RESULT 13
US-09-213-053-8
; Sequence 8, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213,053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; TYPE: DNA
; LENGTH: 33
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
;
US-09-213-053-8

Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
Db      17 GATCGATATCGGCCCA 33

RESULT 14
US-09-213-053-8/c
; Sequence 8, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213,053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
```

```
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-213-053-8
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TGAGACCGATTCGATC 18
DB      33 TGGGCCGATTCATC 17
```

```
RESULT 15
US-09-213-053-9
; Sequence 9, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-213-053-9
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TGAGACCGATTCGATC 18
DB      5 TGGGCCGATTCATC 21
```

```
RESULT 16
US-09-213-053-9/c
; Sequence 9, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
```

```
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-213-053-9
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
DB      21 GATCGATATCGGCCCA 5
```

```
RESULT 17
US-09-213-053-28
; Sequence 28, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-213-053-28
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
DB      23 GATCGATATCGGCCCA 39
```

```
RESULT 18
US-09-213-053-28/c
; Sequence 28, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
```

```

; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-28
```

```

Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      2 TGAGACCGATATCGGTC 18
        ||| ||||| ||||| |||
DB      39 TGGGCCCGATATCGATC 23
```

```

RESULT 19
US-09-213-053-29
; Sequence 29, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-29
```

```

Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      2 TGAGACCGATATCGGTC 18
        ||| ||||| ||||| |||
DB      5 TGGGCCCGATATCGATC 21
```

```

RESULT 20
US-09-213-053-29/C
; Sequence 29, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
```

```

; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-29
```

```

Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      5 GACCGATATCGGTCCTCA 21
        ||| ||||| ||||| |||
DB      21 GATCGATATCGGGCCCA 5
```

```

RESULT 21
US-08-235-503B-68
; Sequence 68, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Baichwal, Vijay R
; APPLICANT: Strulovich, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCE ADDRESSES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHER, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,503B
; FILING DATE: 29-Apr-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-235-503B-68
```

```

Query Match      54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

OY 3 GAGACCGATATCGGTCTC 22
| | | | | | | | | | | | | | | | | | | | | |
Db 6 CTCACACCGATTTCGGTCTC 25

RESULT 22
US-08-235-503B-68/c
Sequence 68, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Balchwal, Vijay R
APPLICANT: Strulovici, Berta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-235-503B-68
Query Match 54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CTGAGACCGATATCGGTCTC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 25 CTCACACCGATTTCGGTCTC 6
US-08-235-503B-69
Sequence 69, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Balchwal, Vijay R
APPLICANT: Strulovici, Berta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs

ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-235-503B-69
Query Match 54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CTGAGACCGATATCGGTCTC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 4 CTCACACCGATTTCGGTCTC 23

RESULT 24
US-08-235-503B-69/c
Sequence 69, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Balchwal, Vijay R
APPLICANT: Strulovici, Berta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-235-503B-69

Query Match 54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAGACGATATCGGTCTCAG 22
Db 23 GTGACCAAAACGGTGTGAG 4

RESULT 25

PCT-US95-05265-68
Sequence 68, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-05265-68

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAGACGATATCGGTCTCAG 22
Db 6 GTGACCAAAACGGTGTGAG 25

RESULT 26

PCT-US95-05265-68/C
Sequence 68, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY

NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-05265-68

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGACACCATATCGGTCTC 20
Db 25 CTCACACCGTTTCGGTCTC 6

RESULT 27

PCT-US95-05265-69
Sequence 69, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910.277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-05265-69

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTC 20
Db 4 CTCACACCGTTTCGTCAC 23

RESULT 28

PCT-US95-05265-69/c
Sequence 69, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embardadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-05265-69

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 3 GAGACGATATCGTCTCAG 22

Db 23 GTGACCGAAAAACGGTGTGAG 4

RESULT 29

US-08-402-964-3
Sequence 3, Application US/08402964
Patent No. 5582993
GENERAL INFORMATION:
APPLICANT: Stackebrandt, Erko
APPLICANT: Lane, David J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
DETECTION OF BACTERIA IN THE GENUS VIBRIO
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,964
FILING DATE: 10-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/138,862
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,785
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Faase, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 01886/051002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-402-964-3

Query Match 54.5%; Score 12; DB 1; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTC 20
Db 17 CGGGAGACGAUACGGCGUC 36

RESULT 30

US-08-402-964-3/c
Sequence 3, Application US/08402964
Patent No. 5582993
GENERAL INFORMATION:
APPLICANT: Stackebrandt, Erko
APPLICANT: Lane, David J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
DETECTION OF BACTERIA IN THE GENUS VIBRIO
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:


```

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,964
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/138,862
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,785
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Faase, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 01886/051002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: RNA
;
; US-08-402-964-3
;
Query Match          54.5%; Score 12; DB 1; Length 37;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GAGACCGATATCGGTCTCAG 22
Db      36 GAGCCGATATCGTTCCCG 17

RESULT 31
; US-09-641-638-720
; Sequence 720, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 720
; LENGTH: 47
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; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-231-100 : polymorphic base C or T
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; US-09-641-638-720
;
Query Match          54.5%; Score 12; DB 4; Length 47;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TGAGACCGATATCGGTCTCA 21
Db      28 TTAACCGAATCGGTCTCA 47

RESULT 32
; US-09-641-638-720/c
; Sequence 720, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 720
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-231-100 : polymorphic base C or T
;
; US-09-641-638-720
;
Query Match          54.5%; Score 12; DB 4; Length 47;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TGAGACCGATATCGGTCTCA 21
Db      47 TGAGACCGATTCGTGTTAA 28

RESULT 33
; US-09-213-053-21
; Sequence 21, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213,053
; CURRENT FILING DATE: 1998-12-16
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EARLIER APPLICATION NUMBER: 9608242
 EARLIER FILING DATE: 1996-06-27
 EARLIER APPLICATION NUMBER: PCT/FR97/01115
 EARLIER FILING DATE: 1997-06-23
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 21
 LENGTH: 34
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: oligonucleotide
 US-09-213-053-21

Query Match 53.6%; Score 11.8; DB 3; Length 34;
 Best Local Similarity 86.7%; Pred. No. 1.6e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TGAGACCGATATCGG 16
 Db 9 TGGGCCCGATATCGG 23

RESULT 34
 US-09-213-053-21/C
 Sequence 21, Application US/09213053
 Patent No. 6159477
 GENERAL INFORMATION:
 APPLICANT: AUDONNET, Jean-Christophe
 APPLICANT: BAUDU, Philippe
 TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
 TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
 TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
 FILE REFERENCE: 454313-2200
 CURRENT APPLICATION NUMBER: US/09/213,053
 CURRENT FILING DATE: 1998-12-16
 EARLIER APPLICATION NUMBER: 9608242
 EARLIER FILING DATE: 1996-06-27
 EARLIER APPLICATION NUMBER: PCT/FR97/01115
 EARLIER FILING DATE: 1997-06-23
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 21
 LENGTH: 34
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: oligonucleotide
 US-09-213-053-21

Query Match 53.6%; Score 11.8; DB 3; Length 34;
 Best Local Similarity 86.7%; Pred. No. 1.6e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 7 CCGATATCGGTCCTCA 21
 Db 23 CCGATATCGGCGCCA 9

RESULT 35
 US-07-967-693-43
 Sequence 43, Application US/07967693
 Patent No. 5494814
 GENERAL INFORMATION:
 APPLICANT: James P. Haseloff
 APPLICANT: Wayne L. Gerlach
 APPLICANT: Philip A. Jennings
 APPLICANT: Fiona H. Cameron
 TITLE OF INVENTION: RIBOZYMES
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, Esq.
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/967,693
 FILING DATE: 19921027
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 40313-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-977-9550
 TELEFAX: 212-664-0525
 TELEX: 422523 coop ui
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA (genomic)
 US-07-967-693-43

Query Match 53.6%; Score 11.8; DB 1; Length 45;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TGAGACCGATATCGG 16
 Db 15 UGAGUCCGATATCGG 29

RESULT 36
 US-07-967-693-43/C
 Sequence 43, Application US/07967693
 Patent No. 5494814
 GENERAL INFORMATION:
 APPLICANT: James P. Haseloff
 APPLICANT: Wayne L. Gerlach
 APPLICANT: Philip A. Jennings
 APPLICANT: Fiona H. Cameron
 TITLE OF INVENTION: RIBOZYMES
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White, Esq.
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/967,693
 FILING DATE: 19921027
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 40313-B
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-07-967-693-43

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 CCGATATCGGTCTCA 21
DB 29 CGGATATCGACTCA 15

RESULT 37
US-08-195-072-41
Sequence 41, Application US/08195072
Patent No. 5543508
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,072
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-072-41

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TGAGCCGATATCGG 16
DB 15 UGAGUCCGATATCGG 29

RESULT 38
US-08-195-072-41/c
Sequence 41, Application US/08195072
Patent No. 5543508
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,072
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-072-41

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 CCGATATCGGTCTCA 21
DB 29 CGGATATCGACTCA 15

RESULT 39
US-08-195-735-41
Sequence 41, Application US/08195735
Patent No. 5574143
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,735
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-735-41

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGG 16
DB 15 UGAGUCCGATATCCG 29

RESULT 40
US-08-195-735-41/c
Sequence 41, Application US/08195735
Patent No. 5574143
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,735
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-735-41

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 CGGATATCGATCTCA 21
DB 29 CGGATATCGACTCA 15

Search completed: June 14, 2003, 22:39:03
Job time : 73 secs

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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 22:26:30 ; Search time 118 Seconds
(without alignments)
269.977 Million cell updates/sec

Title: US-09-532-001-1
Perfect score: 22
Sequence: 1 CTGAGACCGATATCGTCTCAG 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 826456

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 1000 summaries

Database :

Published Applications_NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	14	63.6	25	9	US-10-098-263B-70455
4	14	63.6	25	9	US-10-098-263B-70455
5	14	63.6	25	9	US-10-098-263B-87625
6	14	63.6	25	9	US-10-098-263B-87625
7	14	63.6	25	9	US-10-098-263B-105385
8	14	63.6	25	9	US-10-098-263B-105385
9	14	63.6	25	9	US-10-098-263B-67902
10	14	63.6	25	9	US-10-098-263B-67902
11	14	63.6	25	9	US-10-098-263B-93368
12	14	63.6	25	9	US-10-098-263B-93368
13	14	63.6	25	9	US-10-098-263B-42695
14	14	63.6	25	9	US-10-098-263B-42695
15	14	63.6	25	9	US-10-098-263B-83125
16	14	63.6	25	9	US-10-098-263B-83125
17	14	63.6	25	9	US-10-098-263B-83125
18	14	63.6	25	9	US-10-098-263B-83125
19	14	63.6	25	9	US-10-098-263B-83125

20	13	59.1	33	9	US-10-011-931-42	Sequence 42, Appl
21	13	59.1	33	9	US-10-011-931-56	Sequence 56, Appl
22	13	59.1	33	9	US-10-011-931-56	Sequence 56, Appl
23	13	59.1	33	9	US-10-011-931-57	Sequence 57, Appl
24	13	59.1	33	9	US-10-011-931-57	Sequence 57, Appl
25	13	59.1	33	9	US-10-098-263B-60005	Sequence 60005, A
26	12.8	58.2	25	9	US-10-098-263B-60005	Sequence 60005, A
27	12.8	58.2	25	9	US-10-098-263B-88139	Sequence 88139, A
28	12.8	58.2	25	9	US-10-098-263B-88139	Sequence 88139, A
29	12.6	57.3	25	9	US-09-745-317-15	Sequence 15, Appl
30	12.6	57.3	25	9	US-09-745-317-15	Sequence 15, Appl
31	12.6	57.3	25	9	US-10-098-263B-130373	Sequence 130373, A
32	12.6	57.3	25	9	US-10-098-263B-130373	Sequence 130373, A
33	12.4	56.4	25	9	US-10-098-263B-21859	Sequence 21859, A
34	12.4	56.4	25	9	US-10-098-263B-21859	Sequence 21859, A
35	12.4	56.4	25	9	US-10-098-263B-30446	Sequence 30446, A
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39	12.4	56.4	25	9	US-10-098-263B-87626	Sequence 87626, A
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44	12.4	56.4	25	9	US-10-098-263B-105386	Sequence 105386, A
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49	12.2	55.5	25	9	US-10-098-263B-103542	Sequence 103542, A
50	12.2	55.5	25	9	US-10-098-263B-103542	Sequence 103542, A
51	12.2	55.5	25	9	US-10-098-263B-113888	Sequence 113888, A
52	12.2	55.5	25	9	US-10-098-263B-113888	Sequence 113888, A
53	12.2	55.5	31	10	US-09-086-118-18	Sequence 18, Appl
54	12.2	55.5	31	10	US-09-086-118-18	Sequence 18, Appl
55	12.2	55.5	33	9	US-10-085-906-145	Sequence 345, Appl
56	12.2	55.5	33	9	US-10-085-906-145	Sequence 345, Appl
57	12.2	55.5	36	10	US-09-504-231A-1744	Sequence 1744, Appl
58	12.2	55.5	36	10	US-09-504-231A-1744	Sequence 1744, Appl
59	12.2	55.5	36	10	US-09-274-5530-1744	Sequence 1744, Appl
60	12.2	55.5	36	10	US-09-274-5530-1744	Sequence 1744, Appl
61	12.2	55.5	25	9	US-10-215-112-4017	Sequence 4017, Appl
62	12.2	55.5	25	9	US-10-215-112-4017	Sequence 4017, Appl
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64	12.2	55.5	25	9	US-10-098-263B-25135	Sequence 25135, A
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78	12.2	55.5	25	9	US-10-098-263B-92749	Sequence 92749, A
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81	12.2	55.5	25	9	US-10-098-263B-126042	Sequence 126042, A
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83	12.2	55.5	25	9	US-10-098-263B-126320	Sequence 126320, A
84	12.2	55.5	25	9	US-10-098-263B-126320	Sequence 126320, A
85	12.2	55.5	31	9	US-09-288-971-6	Sequence 6, Appl
86	12.2	55.5	31	9	US-09-288-971-6	Sequence 6, Appl
87	12.2	55.5	31	9	US-09-288-971-10	Sequence 10, Appl
88	12.2	55.5	31	9	US-09-288-971-10	Sequence 10, Appl
89	11.8	53.6	25	9	US-10-098-263B-3107	Sequence 3107, Appl
90	11.8	53.6	25	9	US-10-098-263B-3107	Sequence 3107, Appl
91	11.8	53.6	25	9	US-10-098-263B-90489	Sequence 90489, A
92	11.8	53.6	25	9	US-10-098-263B-90489	Sequence 90489, A

93	11.6	52.7	20	9	US-09-864-636A-2346	Sequence 2346, Ap	c 166	11.4	51.8	39	9	US-09-824-017-15	Sequence 15, Appl
94	11.6	52.7	20	9	US-09-864-636A-2346	Sequence 2346, Ap	c 167	11.4	51.8	39	9	US-09-864-636A-2346	Sequence 15, Appl
95	11.6	52.7	21	9	US-09-923-327-61	Sequence 61, Appl	c 168	11.4	51.8	39	9	US-09-923-327-61	Sequence 15, Appl
96	11.6	52.7	21	9	US-09-923-327-61	Sequence 61, Appl	c 169	11.4	51.8	41	10	US-09-965-099-58	Sequence 58, Appl
97	11.6	52.7	25	9	US-10-215-112-3904	Sequence 3904, Ap	c 170	11.4	51.8	41	10	US-09-965-099-58	Sequence 58, Appl
98	11.6	52.7	25	9	US-10-215-112-3904	Sequence 3904, Ap	c 171	11.4	51.8	41	10	US-09-965-099-58	Sequence 58, Appl
99	11.6	52.7	25	9	US-10-098-263B-14263	Sequence 14263, A	c 172	11.4	51.8	41	12	US-10-051-852-58	Sequence 58, Appl
100	11.6	52.7	25	9	US-10-098-263B-14263	Sequence 14263, A	c 173	11.4	51.8	41	12	US-10-051-852-58	Sequence 58, Appl
101	11.6	52.7	25	9	US-10-098-263B-20211	Sequence 20211, A	c 174	11.4	51.8	41	12	US-10-051-852-58	Sequence 58, Appl
102	11.6	52.7	25	9	US-10-098-263B-20211	Sequence 20211, A	c 175	11.4	51.8	41	12	US-10-051-852-58	Sequence 58, Appl
103	11.6	52.7	25	9	US-10-098-263B-42696	Sequence 42696, A	c 176	11.4	51.8	41	12	US-10-051-852-58	Sequence 58, Appl
104	11.6	52.7	25	9	US-10-098-263B-42696	Sequence 42696, A	c 177	11.2	50.9	24	7	US-08-860-844-50	Sequence 50, Appl
105	11.6	52.7	25	9	US-10-098-263B-58389	Sequence 58389, A	c 178	11.2	50.9	24	7	US-08-860-844-50	Sequence 50, Appl
106	11.6	52.7	25	9	US-10-098-263B-58389	Sequence 58389, A	c 179	11.2	50.9	25	9	US-10-215-112-11803	Sequence 11803, A
107	11.6	52.7	25	9	US-10-098-263B-59017	Sequence 59017, A	c 180	11.2	50.9	25	9	US-10-215-112-11803	Sequence 11803, A
108	11.6	52.7	25	9	US-10-098-263B-59017	Sequence 59017, A	c 181	11.2	50.9	25	9	US-10-098-263B-13044	Sequence 13044, A
109	11.6	52.7	25	9	US-10-098-263B-81665	Sequence 81665, A	c 182	11.2	50.9	25	9	US-10-098-263B-13044	Sequence 13044, A
110	11.6	52.7	25	9	US-10-098-263B-81665	Sequence 81665, A	c 183	11.2	50.9	25	9	US-10-098-263B-18710	Sequence 18710, A
111	11.6	52.7	25	9	US-10-098-263B-82202	Sequence 82202, A	c 184	11.2	50.9	25	9	US-10-098-263B-18710	Sequence 18710, A
112	11.6	52.7	25	9	US-10-098-263B-82202	Sequence 82202, A	c 185	11.2	50.9	25	9	US-10-098-263B-18995	Sequence 18995, A
113	11.6	52.7	25	9	US-10-098-263B-82519	Sequence 82519, A	c 186	11.2	50.9	25	9	US-10-098-263B-18995	Sequence 18995, A
114	11.6	52.7	25	9	US-10-098-263B-82519	Sequence 82519, A	c 187	11.2	50.9	25	9	US-10-098-263B-23552	Sequence 23552, A
115	11.6	52.7	25	9	US-10-098-263B-82520	Sequence 82520, A	c 188	11.2	50.9	25	9	US-10-098-263B-23552	Sequence 23552, A
116	11.6	52.7	25	9	US-10-098-263B-82520	Sequence 82520, A	c 189	11.2	50.9	25	9	US-10-098-263B-46294	Sequence 46294, A
117	11.6	52.7	25	9	US-10-098-263B-92137	Sequence 92137, A	c 190	11.2	50.9	25	9	US-10-098-263B-46294	Sequence 46294, A
118	11.6	52.7	25	9	US-10-098-263B-92137	Sequence 92137, A	c 191	11.2	50.9	25	9	US-10-098-263B-47459	Sequence 47459, A
119	11.6	52.7	25	9	US-10-098-263B-92138	Sequence 92138, A	c 192	11.2	50.9	25	9	US-10-098-263B-47459	Sequence 47459, A
120	11.6	52.7	25	9	US-10-098-263B-92138	Sequence 92138, A	c 193	11.2	50.9	25	9	US-10-098-263B-47460	Sequence 47460, A
121	11.6	52.7	25	9	US-10-098-263B-104108	Sequence 104108, A	c 194	11.2	50.9	25	9	US-10-098-263B-47460	Sequence 47460, A
122	11.6	52.7	25	9	US-10-098-263B-104108	Sequence 104108, A	c 195	11.2	50.9	25	9	US-10-098-263B-60006	Sequence 60006, A
123	11.6	52.7	38	9	US-09-780-533A-2952	Sequence 2952, Ap	c 196	11.2	50.9	25	9	US-10-098-263B-60006	Sequence 60006, A
124	11.6	52.7	40	9	US-09-997-931-114	Sequence 114, App	c 197	11.2	50.9	25	9	US-10-098-263B-69137	Sequence 69137, A
125	11.6	52.7	40	9	US-09-997-931-114	Sequence 114, App	c 198	11.2	50.9	25	9	US-10-098-263B-69137	Sequence 69137, A
126	11.6	52.7	40	9	US-10-040-430-44	Sequence 44, Appl	c 199	11.2	50.9	25	9	US-10-098-263B-69138	Sequence 69138, A
127	11.4	51.8	18	9	US-10-040-430-44	Sequence 44, Appl	c 200	11.2	50.9	25	9	US-10-098-263B-69138	Sequence 69138, A
128	11.4	51.8	18	9	US-09-349-058-44	Sequence 44, Appl	c 201	11.2	50.9	25	9	US-10-098-263B-75854	Sequence 75854, A
129	11.4	51.8	18	9	US-09-349-058-44	Sequence 44, Appl	c 202	11.2	50.9	25	9	US-10-098-263B-75854	Sequence 75854, A
130	11.4	51.8	18	9	US-09-349-058-44	Sequence 44, Appl	c 203	11.2	50.9	25	9	US-10-098-263B-76007	Sequence 76007, A
131	11.4	51.8	25	9	US-09-966-880A-16	Sequence 16, Appl	c 204	11.2	50.9	25	9	US-10-098-263B-76007	Sequence 76007, A
132	11.4	51.8	25	9	US-09-966-880A-16	Sequence 16, Appl	c 205	11.2	50.9	25	9	US-10-098-263B-76008	Sequence 76008, A
133	11.4	51.8	25	9	US-10-098-263B-3878	Sequence 3878, Ap	c 206	11.2	50.9	25	9	US-10-098-263B-76008	Sequence 76008, A
134	11.4	51.8	25	9	US-10-098-263B-3878	Sequence 3878, Ap	c 207	11.2	50.9	25	9	US-10-098-263B-88140	Sequence 88140, A
135	11.4	51.8	25	9	US-10-098-263B-11001	Sequence 11001, A	c 208	11.2	50.9	25	9	US-10-098-263B-88140	Sequence 88140, A
136	11.4	51.8	25	9	US-10-098-263B-11001	Sequence 11001, A	c 209	11.2	50.9	25	9	US-10-098-263B-95142	Sequence 95142, A
137	11.4	51.8	25	9	US-10-098-263B-11002	Sequence 11002, A	c 210	11.2	50.9	25	9	US-10-098-263B-95142	Sequence 95142, A
138	11.4	51.8	25	9	US-10-098-263B-11002	Sequence 11002, A	c 211	11.2	50.9	25	9	US-10-098-263B-103599	Sequence 103599, A
139	11.4	51.8	25	9	US-10-098-263B-35948	Sequence 35948, A	c 212	11.2	50.9	25	9	US-10-098-263B-103599	Sequence 103599, A
140	11.4	51.8	25	9	US-10-098-263B-35948	Sequence 35948, A	c 213	11.2	50.9	33	9	US-09-900-590-43	Sequence 43, Appl
141	11.4	51.8	25	9	US-10-098-263B-83126	Sequence 83126, A	c 214	11.2	50.9	33	9	US-09-900-590-43	Sequence 43, Appl
142	11.4	51.8	25	9	US-10-098-263B-83126	Sequence 83126, A	c 215	11.2	50.9	38	9	US-09-877-478-1621	Sequence 3621, Ap
143	11.4	51.8	25	9	US-10-098-263B-88699	Sequence 88699, A	c 216	11.2	50.9	20	10	US-09-441-522-14	Sequence 14, Appl
144	11.4	51.8	25	9	US-10-098-263B-88699	Sequence 88699, A	c 217	11.2	50.9	20	10	US-09-441-522-14	Sequence 14, Appl
145	11.4	51.8	25	9	US-10-098-263B-101532	Sequence 101532, A	c 218	11.2	50.9	20	10	US-10-215-112-1277	Sequence 1277, Ap
146	11.4	51.8	25	9	US-10-098-263B-101532	Sequence 101532, A	c 219	11.2	50.9	25	9	US-10-215-112-1277	Sequence 1277, Ap
147	11.4	51.8	25	9	US-10-098-263B-118692	Sequence 118692, A	c 220	11.2	50.9	25	9	US-10-215-112-1279	Sequence 1279, Ap
148	11.4	51.8	25	9	US-10-098-263B-118692	Sequence 118692, A	c 221	11.2	50.9	25	9	US-10-215-112-1279	Sequence 1279, Ap
149	11.4	51.8	25	9	US-10-098-263B-123691	Sequence 123691, A	c 222	11.2	50.9	25	9	US-10-215-112-1279	Sequence 1279, Ap
150	11.4	51.8	25	9	US-10-098-263B-123691	Sequence 123691, A	c 223	11.2	50.9	25	9	US-10-215-112-1279	Sequence 1279, Ap
151	11.4	51.8	25	9	US-10-098-263B-127919	Sequence 127919, A	c 224	11.2	50.9	25	9	US-10-215-112-10771	Sequence 10771, A
152	11.4	51.8	25	9	US-10-098-263B-127919	Sequence 127919, A	c 225	11.2	50.9	25	9	US-10-215-112-10771	Sequence 10771, A
153	11.4	51.8	29	10	US-09-893-615-84	Sequence 84, Appl	c 226	11.2	50.9	25	9	US-10-215-112-12780	Sequence 12780, A
154	11.4	51.8	29	10	US-09-893-615-84	Sequence 84, Appl	c 227	11.2	50.9	25	9	US-10-215-112-12780	Sequence 12780, A
155	11.4	51.8	29	10	US-09-753-126-54	Sequence 54, Appl	c 228	11.2	50.9	25	9	US-09-940-185-4107	Sequence 4107, Ap
156	11.4	51.8	29	10	US-09-753-126-54	Sequence 54, Appl	c 229	11.2	50.9	25	9	US-09-940-185-4107	Sequence 4107, Ap
157	11.4	51.8	38	9	US-09-966-277-37	Sequence 37, Appl	c 230	11.2	50.9	25	9	US-10-098-263B-6851	Sequence 6851, Ap
158	11.4	51.8	38	9	US-09-966-277-37	Sequence 37, Appl	c 231	11.2	50.9	25	9	US-10-098-263B-6851	Sequence 6851, Ap
159	11.4	51.8	38	9	US-09-966-277-38	Sequence 38, Appl	c 232	11.2	50.9	25	9	US-10-098-263B-6852	Sequence 6852, Ap
160	11.4	51.8	38	9	US-09-966-277-38	Sequence 38, Appl	c 233	11.2	50.9	25	9	US-10-098-263B-6852	Sequence 6852, Ap
161	11.4	51.8	38	9	US-09-966-930-37	Sequence 37, Appl	c 234	11.2	50.9	25	9	US-10-098-263B-7487	Sequence 7487, Ap
162	11.4	51.8	38	9	US-09-966-930-37	Sequence 37, Appl	c 235	11.2	50.9	25	9	US-10-098-263B-7487	Sequence 7487, Ap
163	11.4	51.8	38	9	US-09-966-930-38	Sequence 38, Appl	c 236	11.2	50.9	25	9	US-10-098-263B-7487	Sequence 7487, Ap
164	11.4	51.8	38	9	US-09-966-930-38	Sequence 38, Appl	c 237	11.2	50.9	25	9	US-10-098-263B-7488	Sequence 7488, Ap
165	11.4	51.8	39	9	US-09-824-017-15	Sequence 15, Appl	c 238	11.2	50.9	25	9	US-10-098-263B-7488	Sequence 7488, Ap

C 239	11	50.0	25	9	US-10-098-263B-10947	Sequence 10947, A	C 312	10.8	49.1	25	9	US-10-098-263B-19329	Sequence 19329, A
C 240	11	50.0	25	9	US-10-098-263B-10947	Sequence 10947, A	313	10.8	49.1	25	9	US-10-098-263B-21860	Sequence 21860, A
C 241	11	50.0	25	9	US-10-098-263B-10948	Sequence 10948, A	C 314	10.8	49.1	25	9	US-10-098-263B-21860	Sequence 21860, A
C 242	11	50.0	25	9	US-10-098-263B-10948	Sequence 10948, A	315	10.8	49.1	25	9	US-10-098-263B-25767	Sequence 25767, A
C 243	11	50.0	25	9	US-10-098-263B-14534	Sequence 14534, A	C 316	10.8	49.1	25	9	US-10-098-263B-25767	Sequence 25767, A
C 244	11	50.0	25	9	US-10-098-263B-14534	Sequence 14534, A	317	10.8	49.1	25	9	US-10-098-263B-26347	Sequence 26347, A
C 245	11	50.0	25	9	US-10-098-263B-17340	Sequence 17340, A	C 318	10.8	49.1	25	9	US-10-098-263B-26947	Sequence 26947, A
C 246	11	50.0	25	9	US-10-098-263B-17340	Sequence 17340, A	319	10.8	49.1	25	9	US-10-098-263B-28731	Sequence 28731, A
C 247	11	50.0	25	9	US-10-098-263B-19137	Sequence 19137, A	C 320	10.8	49.1	25	9	US-10-098-263B-28731	Sequence 28731, A
C 248	11	50.0	25	9	US-10-098-263B-19137	Sequence 19137, A	321	10.8	49.1	25	9	US-10-098-263B-35938	Sequence 35938, A
C 249	11	50.0	25	9	US-10-098-263B-23785	Sequence 23785, A	C 322	10.8	49.1	25	9	US-10-098-263B-35938	Sequence 35938, A
C 250	11	50.0	25	9	US-10-098-263B-23785	Sequence 23785, A	323	10.8	49.1	25	9	US-10-098-263B-48087	Sequence 48087, A
C 251	11	50.0	25	9	US-10-098-263B-52290	Sequence 52290, A	C 324	10.8	49.1	25	9	US-10-098-263B-48087	Sequence 48087, A
C 252	11	50.0	25	9	US-10-098-263B-52290	Sequence 52290, A	325	10.8	49.1	25	9	US-10-098-263B-48255	Sequence 48255, A
C 253	11	50.0	25	9	US-10-098-263B-52785	Sequence 52785, A	C 326	10.8	49.1	25	9	US-10-098-263B-48255	Sequence 48255, A
C 254	11	50.0	25	9	US-10-098-263B-52785	Sequence 52785, A	327	10.8	49.1	25	9	US-10-098-263B-53591	Sequence 53591, A
C 255	11	50.0	25	9	US-10-098-263B-57224	Sequence 57224, A	C 328	10.8	49.1	25	9	US-10-098-263B-53591	Sequence 53591, A
C 256	11	50.0	25	9	US-10-098-263B-57224	Sequence 57224, A	329	10.8	49.1	25	9	US-10-098-263B-53831	Sequence 53831, A
C 257	11	50.0	25	9	US-10-098-263B-63312	Sequence 63312, A	C 330	10.8	49.1	25	9	US-10-098-263B-53831	Sequence 53831, A
C 258	11	50.0	25	9	US-10-098-263B-63312	Sequence 63312, A	331	10.8	49.1	25	9	US-10-098-263B-61572	Sequence 61572, A
C 259	11	50.0	25	9	US-10-098-263B-64811	Sequence 64811, A	C 332	10.8	49.1	25	9	US-10-098-263B-61572	Sequence 61572, A
C 260	11	50.0	25	9	US-10-098-263B-64811	Sequence 64811, A	333	10.8	49.1	25	9	US-10-098-263B-61862	Sequence 61862, A
C 261	11	50.0	25	9	US-10-098-263B-66051	Sequence 66051, A	C 334	10.8	49.1	25	9	US-10-098-263B-61862	Sequence 61862, A
C 262	11	50.0	25	9	US-10-098-263B-66051	Sequence 66051, A	335	10.8	49.1	25	9	US-10-098-263B-63695	Sequence 63695, A
C 263	11	50.0	25	9	US-10-098-263B-66052	Sequence 66052, A	C 336	10.8	49.1	25	9	US-10-098-263B-63695	Sequence 63695, A
C 264	11	50.0	25	9	US-10-098-263B-66052	Sequence 66052, A	337	10.8	49.1	25	9	US-10-098-263B-74524	Sequence 74524, A
C 265	11	50.0	25	9	US-10-098-263B-66864	Sequence 66864, A	C 338	10.8	49.1	25	9	US-10-098-263B-74524	Sequence 74524, A
C 266	11	50.0	25	9	US-10-098-263B-68684	Sequence 68684, A	339	10.8	49.1	25	9	US-10-098-263B-79851	Sequence 79851, A
C 267	11	50.0	25	9	US-10-098-263B-71442	Sequence 71442, A	C 340	10.8	49.1	25	9	US-10-098-263B-79851	Sequence 79851, A
C 268	11	50.0	25	9	US-10-098-263B-71442	Sequence 71442, A	341	10.8	49.1	25	9	US-10-098-263B-99205	Sequence 99205, A
C 269	11	50.0	25	9	US-10-098-263B-72969	Sequence 72969, A	C 342	10.8	49.1	25	9	US-10-098-263B-99205	Sequence 99205, A
C 270	11	50.0	25	9	US-10-098-263B-87337	Sequence 87337, A	C 343	10.8	49.1	25	9	US-10-098-263B-101400	Sequence 101400, A
C 271	11	50.0	25	9	US-10-098-263B-87337	Sequence 87337, A	C 344	10.8	49.1	25	9	US-10-098-263B-101400	Sequence 101400, A
C 272	11	50.0	25	9	US-10-098-263B-87338	Sequence 87338, A	345	10.8	49.1	25	9	US-10-098-263B-101571	Sequence 101571, A
C 273	11	50.0	25	9	US-10-098-263B-87338	Sequence 87338, A	C 346	10.8	49.1	25	9	US-10-098-263B-101571	Sequence 101571, A
C 274	11	50.0	25	9	US-10-098-263B-87338	Sequence 87338, A	347	10.8	49.1	25	9	US-10-098-263B-107450	Sequence 107450, A
C 275	11	50.0	25	9	US-10-098-263B-101699	Sequence 101699, A	C 348	10.8	49.1	25	9	US-10-098-263B-107450	Sequence 107450, A
C 276	11	50.0	25	9	US-10-098-263B-101699	Sequence 101699, A	349	10.8	49.1	25	9	US-10-098-263B-109684	Sequence 109684, A
C 277	11	50.0	25	9	US-10-098-263B-101700	Sequence 101700, A	C 350	10.8	49.1	25	9	US-10-098-263B-109684	Sequence 109684, A
C 278	11	50.0	25	9	US-10-098-263B-101700	Sequence 101700, A	351	10.8	49.1	25	9	US-10-098-263B-110252	Sequence 110252, A
C 279	11	50.0	25	9	US-10-098-263B-115034	Sequence 115034, A	C 352	10.8	49.1	25	9	US-10-098-263B-110252	Sequence 110252, A
C 280	11	50.0	25	9	US-10-098-263B-115034	Sequence 115034, A	353	10.8	49.1	25	9	US-10-098-263B-124541	Sequence 124541, A
C 281	11	50.0	25	9	US-10-098-263B-120179	Sequence 120179, A	C 354	10.8	49.1	25	9	US-10-098-263B-124542	Sequence 124542, A
C 282	11	50.0	25	9	US-10-098-263B-120179	Sequence 120179, A	355	10.8	49.1	25	9	US-10-098-263B-124542	Sequence 124542, A
C 283	11	50.0	25	9	US-10-098-263B-120180	Sequence 120180, A	C 356	10.8	49.1	25	9	US-10-098-263B-125766	Sequence 125766, A
C 284	11	50.0	25	9	US-10-098-263B-120180	Sequence 120180, A	357	10.8	49.1	25	9	US-10-098-263B-125766	Sequence 125766, A
C 285	11	50.0	25	9	US-10-098-263B-121579	Sequence 121579, A	C 358	10.8	49.1	25	9	US-10-098-263B-125766	Sequence 125766, A
C 286	11	50.0	25	9	US-10-098-263B-121579	Sequence 121579, A	359	10.8	49.1	32	9	US-10-282-602-5	Sequence 5, Appl1
C 287	11	50.0	25	9	US-10-098-263B-121684	Sequence 121684, A	C 360	10.8	49.1	32	9	US-10-282-602-5	Sequence 5, Appl1
C 288	11	50.0	25	9	US-10-098-263B-121684	Sequence 121684, A	361	10.8	49.1	35	9	US-10-194-594-3	Sequence 3, Appl1
C 289	11	50.0	25	9	US-10-098-263B-129558	Sequence 129558, A	C 362	10.8	49.1	35	9	US-10-194-594-3	Sequence 3, Appl1
C 290	11	50.0	25	9	US-10-098-263B-129558	Sequence 129558, A	363	10.8	49.1	38	9	US-09-997-468A-3	Sequence 3, Appl1
C 291	11	50.0	25	9	US-10-098-263B-130374	Sequence 130374, A	C 364	10.8	49.1	38	9	US-09-997-468A-3	Sequence 3, Appl1
C 292	11	50.0	25	9	US-10-098-263B-130374	Sequence 130374, A	365	10.8	49.1	48	10	US-09-464-767-2	Sequence 2, Appl1
C 293	11	50.0	37	9	US-10-036-949-56	Sequence 56, Appl1	C 366	10.8	48.2	17	9	US-09-464-767-2	Sequence 2, Appl1
C 294	11	50.0	37	9	US-10-036-949-56	Sequence 56, Appl1	367	10.6	48.2	17	9	US-09-864-636A-1830	Sequence 1830, Ap1
C 295	11	50.0	37	9	US-10-002-720-9	Sequence 9, Appl1	C 368	10.6	48.2	17	9	US-09-864-636A-1830	Sequence 1830, Ap1
C 296	11	50.0	37	9	US-10-002-720-9	Sequence 9, Appl1	369	10.6	48.2	20	10	US-09-735-995-86	Sequence 86, Appl1
C 297	11	50.0	38	9	US-10-235-618A-7	Sequence 7, Appl1	C 370	10.6	48.2	20	10	US-09-735-995-86	Sequence 86, Appl1
C 298	11	50.0	38	9	US-10-235-618A-7	Sequence 7, Appl1	371	10.6	48.2	24	9	US-09-940-185-1243	Sequence 1243, Ap1
C 299	11	50.0	46	9	US-09-860-738C-75	Sequence 75, Appl1	C 372	10.6	48.2	24	9	US-09-940-185-1243	Sequence 1243, Ap1
C 300	11	50.0	46	9	US-09-860-738C-75	Sequence 75, Appl1	373	10.6	48.2	24	9	US-10-011-855-3	Sequence 3, Appl1
C 301	11	50.0	46	9	US-09-860-738C-80	Sequence 80, Appl1	C 374	10.6	48.2	24	9	US-10-011-855-3	Sequence 3, Appl1
C 302	11	50.0	46	9	US-09-860-738C-80	Sequence 80, Appl1	375	10.6	48.2	24	9	US-10-011-855-7	Sequence 7, Appl1
C 303	11	50.0	48	9	US-09-938-433-15	Sequence 15, Appl1	C 376	10.6	48.2	24	9	US-10-011-855-7	Sequence 7, Appl1
C 304	11	50.0	48	9	US-09-938-433-15	Sequence 15, Appl1	377	10.6	48.2	25	9	US-10-215-112-735	Sequence 75, App
C 305	11	50.0	48	10	US-09-788-209A-15	Sequence 15, Appl1	C 378	10.6	48.2	25	9	US-10-215-112-735	Sequence 75, App
C 306	11	50.0	48	10	US-09-788-209A-15	Sequence 15, Appl1	379	10.6	48.2	25	9	US-10-215-112-735	Sequence 75, App
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C 310	10.8	49.1	25	9	US-10-215-112-10329	Sequence 10329, A	383	10.6	48.2	25	9	US-10-215-112-14421	Sequence 14421, A
C 311	10.8	49.1	25	9	US-10-098-263B-19329	Sequence 19329, A	C 384	10.6	48.2	25	9	US-10-215-112-14421	Sequence 14421, A

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C 388	10.6	48.2	25	US-10-098-263B-5243	Sequence 5243, Ap	C 461	10.6	48.2	25	US-10-098-263B-114799	Sequence 114799, Ap
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C 391	10.6	48.2	25	US-10-098-263B-15179	Sequence 15179, Ap	C 464	10.6	48.2	25	US-10-098-263B-114800	Sequence 114800, Ap
C 392	10.6	48.2	25	US-10-098-263B-15179	Sequence 15179, Ap	C 465	10.6	48.2	25	US-10-098-263B-115255	Sequence 115255, Ap
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C 394	10.6	48.2	25	US-10-098-263B-17254	Sequence 17254, Ap	C 467	10.6	48.2	25	US-10-098-263B-115256	Sequence 115256, Ap
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C 399	10.6	48.2	25	US-10-098-263B-37937	Sequence 37937, Ap	C 472	10.6	48.2	25	US-10-098-263B-120718	Sequence 120718, Ap
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C 401	10.6	48.2	25	US-10-098-263B-38165	Sequence 38165, Ap	C 474	10.6	48.2	25	US-10-098-263B-126450	Sequence 126450, Ap
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C 408	10.6	48.2	25	US-10-098-263B-58373	Sequence 58373, Ap	C 481	10.6	48.2	25	US-10-098-263B-128879	Sequence 128879, Ap
C 409	10.6	48.2	25	US-10-098-263B-58374	Sequence 58374, Ap	C 482	10.6	48.2	25	US-10-098-263B-128879	Sequence 128879, Ap
C 410	10.6	48.2	25	US-10-098-263B-58374	Sequence 58374, Ap	C 483	10.6	48.2	25	US-10-098-263B-128880	Sequence 128880, Ap
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C 413	10.6	48.2	25	US-10-098-263B-66667	Sequence 66667, Ap	C 486	10.6	48.2	30	US-10-011-635A-4	Sequence 4, Appl1
C 414	10.6	48.2	25	US-10-098-263B-66667	Sequence 66667, Ap	C 487	10.6	48.2	31	US-10-017-721-8	Sequence 8, Appl1
C 415	10.6	48.2	25	US-10-098-263B-67925	Sequence 67925, Ap	C 488	10.6	48.2	31	US-10-017-721-8	Sequence 8, Appl1
C 416	10.6	48.2	25	US-10-098-263B-67925	Sequence 67925, Ap	C 489	10.6	48.2	34	US-10-138-838-4	Sequence 4, Appl1
C 417	10.6	48.2	25	US-10-098-263B-67925	Sequence 67925, Ap	C 490	10.6	48.2	34	US-10-138-838-4	Sequence 4, Appl1
C 418	10.6	48.2	25	US-10-098-263B-67926	Sequence 67926, Ap	C 491	10.6	48.2	34	US-10-138-838-4	Sequence 4, Appl1
C 419	10.6	48.2	25	US-10-098-263B-68013	Sequence 68013, Ap	C 492	10.6	48.2	34	US-10-138-838-4	Sequence 4, Appl1
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C 421	10.6	48.2	25	US-10-098-263B-68170	Sequence 68170, Ap	C 494	10.6	48.2	34	US-10-138-905-4	Sequence 4, Appl1
C 422	10.6	48.2	25	US-10-098-263B-68170	Sequence 68170, Ap	C 495	10.6	48.2	34	US-10-138-905-4	Sequence 4, Appl1
C 423	10.6	48.2	25	US-10-098-263B-75129	Sequence 75129, Ap	C 496	10.6	48.2	34	US-10-138-916-4	Sequence 4, Appl1
C 424	10.6	48.2	25	US-10-098-263B-75129	Sequence 75129, Ap	C 497	10.6	48.2	34	US-09-976-800-4	Sequence 4, Appl1
C 425	10.6	48.2	25	US-10-098-263B-75130	Sequence 75130, Ap	C 498	10.6	48.2	34	US-09-976-800-4	Sequence 4, Appl1
C 426	10.6	48.2	25	US-10-098-263B-75130	Sequence 75130, Ap	C 499	10.6	48.2	34	US-10-234-007-18	Sequence 18, Appl1
C 427	10.6	48.2	25	US-10-098-263B-75663	Sequence 75663, Ap	C 500	10.6	48.2	34	US-10-234-007-18	Sequence 18, Appl1
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C 429	10.6	48.2	25	US-10-098-263B-75998	Sequence 75998, Ap	C 502	10.6	48.2	36	US-09-504-231A-1767	Sequence 1767, Ap
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C 431	10.6	48.2	25	US-10-098-263B-81003	Sequence 81003, Ap	C 504	10.6	48.2	36	US-09-504-231A-2403	Sequence 2403, Ap
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C 434	10.6	48.2	25	US-10-098-263B-81450	Sequence 81450, Ap	C 507	10.6	48.2	36	US-09-274-553D-1767	Sequence 1767, Ap
C 435	10.6	48.2	25	US-10-098-263B-82989	Sequence 82989, Ap	C 508	10.6	48.2	36	US-09-274-553D-2403	Sequence 2403, Ap
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C 437	10.6	48.2	25	US-10-098-263B-83528	Sequence 83528, Ap	C 510	10.6	48.2	37	US-09-778-168-16	Sequence 16, Appl1
C 438	10.6	48.2	25	US-10-098-263B-83528	Sequence 83528, Ap	C 511	10.6	48.2	37	US-09-778-175-16	Sequence 16, Appl1
C 439	10.6	48.2	25	US-10-098-263B-84097	Sequence 84097, Ap	C 512	10.6	48.2	37	US-09-778-175-16	Sequence 16, Appl1
C 440	10.6	48.2	25	US-10-098-263B-84097	Sequence 84097, Ap	C 513	10.6	48.2	37	US-09-335-218-16	Sequence 16, Appl1
C 441	10.6	48.2	25	US-10-098-263B-86270	Sequence 86270, Ap	C 514	10.6	48.2	37	US-09-335-218-16	Sequence 16, Appl1
C 442	10.6	48.2	25	US-10-098-263B-86270	Sequence 86270, Ap	C 515	10.6	48.2	38	US-09-864-785-754	Sequence 754, Appl1
C 443	10.6	48.2	25	US-10-098-263B-90294	Sequence 90294, Ap	C 516	10.6	48.2	38	US-09-864-785-754	Sequence 754, Appl1
C 444	10.6	48.2	25	US-10-098-263B-90294	Sequence 90294, Ap	C 517	10.6	48.2	38	US-09-864-785-824	Sequence 824, Appl1
C 445	10.6	48.2	25	US-10-098-263B-90837	Sequence 90837, Ap	C 518	10.6	48.2	38	US-09-864-785-824	Sequence 824, Appl1
C 446	10.6	48.2	25	US-10-098-263B-90837	Sequence 90837, Ap	C 519	10.6	48.2	38	US-09-780-533A-1220	Sequence 1220, Ap
C 447	10.6	48.2	25	US-10-098-263B-99766	Sequence 99766, Ap	C 520	10.6	48.2	38	US-09-780-533A-1220	Sequence 1220, Ap
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C 452	10.6	48.2	25	US-10-098-263B-105403	Sequence 105403, Ap	C 525	10.6	48.2	38	US-09-848-754A-1106	Sequence 1106, Ap
C 453	10.6	48.2	25	US-10-098-263B-105403	Sequence 105403, Ap	C 526	10.6	48.2	38	US-09-848-754A-1397	Sequence 1397, Ap
C 454	10.6	48.2	25	US-10-098-263B-108259	Sequence 108259, Ap	C 527	10.6	48.2	38	US-09-848-754A-1397	Sequence 1397, Ap
C 455	10.6	48.2	25	US-10-098-263B-108259	Sequence 108259, Ap	C 528	10.6	48.2	38	US-09-848-754A-4817	Sequence 4817, Ap
C 456	10.6	48.2	25	US-10-098-263B-113887	Sequence 113887, Ap	C 529	10.6	48.2	38	US-09-848-754A-4817	Sequence 4817, Ap
C 457	10.6	48.2	25	US-10-098-263B-113887	Sequence 113887, Ap	C 530	10.6	48.2	38	US-09-848-754A-5441	Sequence 5441, Ap
C 458	10.6	48.2	25	US-10-098-263B-114619	Sequence 114619, Ap	C 531	10.6	48.2	38	US-09-848-754A-5441	Sequence 5441, Ap

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C 535	10.6	48.2	38	9	US-09-848-754A-5567	Sequence 5567, Ap	C 608	10.4	47.3	25	9	US-10-098-263B-35412	Sequence 35412, A
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C 541	10.6	48.2	39	9	US-09-500-700-46	Sequence 46, Appl1	C 614	10.4	47.3	25	9	US-10-098-263B-44740	Sequence 44740, A
C 542	10.6	48.2	39	9	US-09-500-700-46	Sequence 46, Appl1	C 615	10.4	47.3	25	9	US-10-098-263B-57750	Sequence 57750, A
C 543	10.6	48.2	43	9	US-10-193-960-57	Sequence 57, Appl1	C 616	10.4	47.3	25	9	US-10-098-263B-57750	Sequence 57750, A
C 544	10.6	48.2	43	9	US-10-193-960-57	Sequence 57, Appl1	C 617	10.4	47.3	25	9	US-10-098-263B-58103	Sequence 58103, A
C 545	10.6	48.2	44	10	US-09-896-888A-2	Sequence 2, Appl1	C 618	10.4	47.3	25	9	US-10-098-263B-58103	Sequence 58103, A
C 546	10.6	48.2	44	10	US-09-896-888A-2	Sequence 2, Appl1	C 619	10.4	47.3	25	9	US-10-098-263B-62610	Sequence 62610, A
C 547	10.6	48.2	45	9	US-10-007-132-12	Sequence 12, Appl1	C 620	10.4	47.3	25	9	US-10-098-263B-62610	Sequence 62610, A
C 548	10.6	48.2	45	9	US-10-007-132-12	Sequence 12, Appl1	C 621	10.4	47.3	25	9	US-10-098-263B-62772	Sequence 62772, A
C 549	10.6	48.2	45	9	US-09-771-287-12	Sequence 12, Appl1	C 622	10.4	47.3	25	9	US-10-098-263B-62772	Sequence 62772, A
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C 551	10.4	47.3	22	10	US-09-797-858-2	Sequence 2, Appl1	C 624	10.4	47.3	25	9	US-10-098-263B-67859	Sequence 67859, A
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C 553	10.4	47.3	23	9	US-09-816-814-19	Sequence 19, Appl1	C 626	10.4	47.3	25	9	US-10-098-263B-70148	Sequence 70148, A
C 554	10.4	47.3	23	9	US-09-816-814-19	Sequence 19, Appl1	C 627	10.4	47.3	25	9	US-10-098-263B-70774	Sequence 70774, A
C 555	10.4	47.3	24	7	US-08-964-716-30	Sequence 30, Appl1	C 628	10.4	47.3	25	9	US-10-098-263B-70774	Sequence 70774, A
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C 558	10.4	47.3	24	9	US-09-888-326-806	Sequence 806, App	C 631	10.4	47.3	25	9	US-10-098-263B-74577	Sequence 74577, A
C 559	10.4	47.3	24	9	US-10-112-653-808	Sequence 808, App	C 632	10.4	47.3	25	9	US-10-098-263B-74577	Sequence 74577, A
C 560	10.4	47.3	24	9	US-10-112-653-808	Sequence 808, App	C 633	10.4	47.3	25	9	US-10-098-263B-82867	Sequence 82867, A
C 561	10.4	47.3	24	9	US-10-017-995-837	Sequence 837, App	C 634	10.4	47.3	25	9	US-10-098-263B-82867	Sequence 82867, A
C 562	10.4	47.3	24	9	US-10-017-995-837	Sequence 837, App	C 635	10.4	47.3	25	9	US-10-098-263B-88700	Sequence 88700, A
C 563	10.4	47.3	24	9	US-09-776-479-837	Sequence 837, App	C 636	10.4	47.3	25	9	US-10-098-263B-88700	Sequence 88700, A
C 564	10.4	47.3	24	9	US-09-776-479-837	Sequence 837, App	C 637	10.4	47.3	25	9	US-10-098-263B-92750	Sequence 92750, A
C 565	10.4	47.3	24	9	US-09-940-185-3790	Sequence 3790, App	C 638	10.4	47.3	25	9	US-10-098-263B-92750	Sequence 92750, A
C 566	10.4	47.3	24	9	US-09-940-185-3790	Sequence 3790, App	C 639	10.4	47.3	25	9	US-10-098-263B-94250	Sequence 94250, A
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C 569	10.4	47.3	25	9	US-10-215-112-4140	Sequence 4140, App	C 642	10.4	47.3	25	9	US-10-098-263B-95835	Sequence 95835, A
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C 577	10.4	47.3	25	9	US-10-215-112-13233	Sequence 13233, A	C 650	10.4	47.3	25	9	US-10-098-263B-121816	Sequence 121816, A
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C 589	10.4	47.3	25	9	US-10-098-263B-11518	Sequence 11518, A	C 662	10.4	47.3	25	10	US-09-887-576-535	Sequence 535, App
C 590	10.4	47.3	25	9	US-10-098-263B-11518	Sequence 11518, A	C 663	10.4	47.3	25	9	US-09-844-517-12	Sequence 12, Appl1
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C 593	10.4	47.3	25	9	US-10-098-263B-19164	Sequence 19164, A	C 666	10.4	47.3	25	9	US-10-195-752-18	Sequence 18, Appl1
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C 595	10.4	47.3	25	9	US-10-098-263B-19768	Sequence 19768, A	C 668	10.4	47.3	25	9	US-10-265-713-6	Sequence 6, Appl1
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C 597	10.4	47.3	25	9	US-10-098-263B-25136	Sequence 25136, A	C 670	10.4	47.3	25	10	US-09-764-304-6	Sequence 6, Appl1
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C 601	10.4	47.3	25	9	US-10-098-263B-32765	Sequence 32765, A	C 674	10.4	47.3	25	10	US-09-753-436-31	Sequence 31, Appl1
C 602	10.4	47.3	25	9	US-10-098-263B-32765	Sequence 32765, A	C 675	10.4	47.3	25	10	US-09-253-794-41	Sequence 41, Appl1
C 603	10.4	47.3	25	9	US-10-098-263B-32766	Sequence 32766, A	C 676	10.4	47.3	25	10	US-09-253-794-41	Sequence 41, Appl1

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c 973 10 45.5 25 9 US-09-754-853A-697 Sequence 697, App
c 974 10 45.5 25 9 US-09-754-853A-697 Sequence 697, App
c 975 10 45.5 25 9 US-10-215-112-3778 Sequence 3778, Ap
c 976 10 45.5 25 9 US-10-215-112-3778 Sequence 3778, Ap
c 977 10 45.5 25 9 US-10-215-112-1801 Sequence 11801, A
c 978 10 45.5 25 9 US-10-215-112-1801 Sequence 11801, A
c 979 10 45.5 25 9 US-10-215-112-1262 Sequence 1262, A
c 980 10 45.5 25 9 US-10-215-112-1262 Sequence 1262, A
c 981 10 45.5 25 9 US-10-215-112-12514 Sequence 12514, A
c 982 10 45.5 25 9 US-10-215-112-12514 Sequence 12514, A
c 983 10 45.5 25 9 US-10-215-112-12640 Sequence 12640, A
c 984 10 45.5 25 9 US-10-215-112-12640 Sequence 12640, A
c 985 10 45.5 25 9 US-10-215-112-13726 Sequence 13726, A
c 986 10 45.5 25 9 US-10-215-112-13726 Sequence 13726, A
c 987 10 45.5 25 9 US-10-215-112-14274 Sequence 14274, A
c 988 10 45.5 25 9 US-10-215-112-14274 Sequence 14274, A
c 989 10 45.5 25 9 US-10-215-112-14400 Sequence 14400, A
c 990 10 45.5 25 9 US-10-215-112-14400 Sequence 14400, A
c 991 10 45.5 25 9 US-09-940-185-4580 Sequence 4580, Ap
c 992 10 45.5 25 9 US-09-940-185-4580 Sequence 4580, Ap
c 993 10 45.5 25 9 US-10-098-263B-3530 Sequence 3530, Ap
c 994 10 45.5 25 9 US-10-098-263B-3530 Sequence 3530, Ap
c 995 10 45.5 25 9 US-10-098-263B-5439 Sequence 5439, Ap
c 996 10 45.5 25 9 US-10-098-263B-5439 Sequence 5439, Ap
c 997 10 45.5 25 9 US-10-098-263B-6203 Sequence 6203, Ap
c 998 10 45.5 25 9 US-10-098-263B-6203 Sequence 6203, Ap
c 999 10 45.5 25 9 US-10-098-263B-7969 Sequence 7969, Ap
c1000 10 45.5 25 9 US-10-098-263B-7969 Sequence 7969, Ap
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ALIGNMENTS

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RESULT 1
US-10-098-263B-30445
; Sequence 30445, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
RESULT 2
US-10-098-263B-30445/c
; Sequence 30445, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
```

```
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
RESULT 3
US-10-098-263B-70455
; Sequence 70455, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 4
US-10-098-263B-70455/c
; Sequence 70455, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATC 14
|||
Db 18 CTGAGACCGATATC 5

RESULT 5

US-10-098-263B-87625
; Sequence 87625, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
|||
Db 2 CTGATACCAATATGAGTCTCG 23

RESULT 6

US-10-098-263B-87625/c
; Sequence 87625, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
|||
Db 23 CGGAGACTCATATGCTATCAG 2

RESULT 7

US-10-098-263B-105385
; Sequence 105385, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GATATCGGTCTCAG 22
|||
Db 1 GATATCGGTCTCAG 14

RESULT 8

US-10-098-263B-105385/c
; Sequence 105385, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATC 14
|||
Db 14 CTGAGACCGATATC 1

RESULT 9

US-10-098-263B-67902
; Sequence 67902, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTC 20
Db 4 CGGACGACGATTTCCGTCCG 23

RESULT 10

US-10-098-263B-67902/c
; Sequence 67902, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Beat Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GAGACCGATATCGTCTCAG 22
Db 23 GCGACGGAATCTGTCTCCG 4

RESULT 11

US-10-098-263B-93368
; Sequence 93368, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Beat Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTC 20
Db 2 CGGACGACGATTTCCGTCCG 21

RESULT 12

US-10-098-263B-93368/c
; Sequence 93368, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Beat Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GAGACCGATATCGTCTCAG 22
Db 21 GCGACGGAATCTGTCTCCG 2

RESULT 13

US-10-098-263B-42695
; Sequence 42695, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 42695
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-42695

Query Match 60.0%; Score 13.2; DB 9; Length 25;
Beat Local Similarity 83.3%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 GACCGATATCGTCTCAG 22
Db 1 GACGACATCGTCTCTG 18

RESULT 14

US-10-098-263B-42695/c
; Sequence 42695, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 42695
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-42695

Query Match 60.0%; Score 13.2; DB 9; Length 25;
Beat Local Similarity 83.3%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTC 18
Db 18 CAGAGACCGATATCGGTC 1

RESULT 15
US-10-098-263B-83125

; Sequence 83125, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mitman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 83125

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

Query Match 59.1%; Score 13; DB 9; Length 25;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCGAG 22
Db 3 TGACACCCCTATAGGTCGCCG 23

RESULT 16

US-10-098-263B-83125/c

; Sequence 83125, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mitman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 83125

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

Query Match 59.1%; Score 13; DB 9; Length 25;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTC 21
Db 23 CGGAGACCTATAGGGGTCTCA 3

RESULT 17

US-10-011-931-41

; Sequence 41, Application US/10011931

; Publication No. US20030026806A1

; GENERAL INFORMATION:

; APPLICANT: WITTE, ALISON

; APPLICANT: VARNUM, BRIAN C.

; APPLICANT: QIAN, ZUEMING

; APPLICANT: VEZINA, CHRIS

; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING OF IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF

; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF

; FILE REFERENCE: A-731

; CURRENT APPLICATION NUMBER: US/10/011,931

; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: US 60/244,118

; PRIOR FILING DATE: 2000-10-27

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 41

; LENGTH: 33

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE

US-10-011-931-41

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCGAG 22
Db 3 TGAGAGTGAGTCGTCGCCG 23

RESULT 18
US-10-011-931-41/c

; Sequence 41, Application US/10011931

; Publication No. US20030026806A1

; GENERAL INFORMATION:

; APPLICANT: WITTE, ALISON

; APPLICANT: VARNUM, BRIAN C.

; APPLICANT: QIAN, ZUEMING

; APPLICANT: VEZINA, CHRIS

; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING OF IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF

; FILE REFERENCE: A-731

; CURRENT APPLICATION NUMBER: US/10/011,931

; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: US 60/244,118

; PRIOR FILING DATE: 2000-10-27

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 41

; LENGTH: 33

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE

US-10-011-931-41

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTC 21
Db 23 CTGGGACCGACTTACTCTCA 3

RESULT 19
US-10-011-931-42

; Sequence 42, Application US/10011931

; Publication No. US20030026806A1

; GENERAL INFORMATION:

; APPLICANT: WITTE, ALISON

; APPLICANT: VARNUM, BRIAN C.

; APPLICANT: QIAN, ZUEMING

; APPLICANT: VEZINA, CHRIS

; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING OF IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF

; FILE REFERENCE: A-731

; CURRENT APPLICATION NUMBER: US/10/011,931

```

; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-42

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGGTCTCA 21
    ||| ||| ||| ||| ||| |||
Db 8 CTGGAGCCGACTTCACTCTCA 28

RESULT 20
US-10-011-931-42/c
; Sequence 42, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-42

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 TGAGACCGATATCGGTCTCAG 22
    ||| ||| ||| ||| ||| |||
Db 28 TGAGAGTGAAGTCGCTCCAG 8

RESULT 21
US-10-011-931-56
; Sequence 56, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
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; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-56

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 TGAGACCGATATCGGTCTCAG 22
    ||| ||| ||| ||| ||| |||
Db 3 TGAGAGTGAAGTCGCTCCAG 23

RESULT 22
US-10-011-931-56/c
; Sequence 56, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BI
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-56

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGGTCTCA 21
    ||| ||| ||| ||| ||| |||
Db 23 CTGGAGCCGACTTCACTCTCA 3

RESULT 23
US-10-011-931-57
; Sequence 57, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BI
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
```


LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-57

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCTCA 21
Db 8 CTGGAGCGAGCTTCACTCTCA 28

RESULT 24
US-10-011-931-57/c
Sequence 57, Application US/10011931
Publication No. US20030026806A1
GENERAL INFORMATION:
APPLICANT: WITTE, ALISON
APPLICANT: VANUM, BRIAN C.
APPLICANT: QIAN, ZUENING
APPLICANT: VEZINA, CHRIS
TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
FILE REFERENCE: A-731
CURRENT APPLICATION NUMBER: US/10/011,931
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 60/244,118
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-57

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCTCAG 22
Db 28 TGAGAGTGAAGTCGTCCTCCAG 8

RESULT 25
US-10-098-263B-60005
Sequence 60005, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 60005
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-60005

Query Match 58.2%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 6 ACCGATATCGGTCTCA 21
Db 5 ACCGATATCGGTCTCA 20

RESULT 26
US-10-098-263B-60005/c
Sequence 60005, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 60005
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-60005

Query Match 58.2%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGT 17
Db 20 TGAGATCATGTCGT 5

RESULT 27
US-10-098-263B-88139
Sequence 88139, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 88139
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-88139

Query Match 58.2%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 GACCGATATCGGTCTC 20
Db 7 GACCGATATCGGTCTC 22

RESULT 28
US-10-098-263B-88139/c
Sequence 88139, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1

```
;; CURRENT APPLICATION NUMBER: US/10/098,263B
;; CURRENT FILING DATE: 2003-01-08
;; PRIOR APPLICATION NUMBER: 60/276,759
;; PRIOR FILING DATE: 2001-03-16
;; NUMBER OF SEQ ID NOS: 131066
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 88139
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-10-098-263B-88139
```

```
Query Match          58.2%; Score 12.6; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      3 GAGACCGATATCGGTC 18
        |||||
Db      22 GAGACCGATATCGGTC 7
```

```
RESULT 29
US-09-745-317-15
; Sequence 15, Application US/09745317
; Publication No. US20020187470A1
; GENERAL INFORMATION:
; APPLICANT: Casey, Warren
; APPLICANT: Chen, Jingwen
; APPLICANT: Much, Heidi
; APPLICANT: Taylor, David
; APPLICANT: Weiner, Michael Philip
; TITLE OF INVENTION: DETECTION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 07083, 000602
; CURRENT APPLICATION NUMBER: US/09/745,317
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/173,268
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20020187470A1e =
US-09-745-317-15
```

```
Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      3 GAGACCGATATCGGTC 21
        |||||
Db      5 GATACCGATCTCGGCCCA 23
```

```
RESULT 30
US-09-745-317-15/c
; Sequence 15, Application US/09745317
; Publication No. US20020187470A1
; GENERAL INFORMATION:
; APPLICANT: Casey, Warren
; APPLICANT: Chen, Jingwen
; APPLICANT: Much, Heidi
; APPLICANT: Taylor, David
; APPLICANT: Weiner, Michael Philip
; TITLE OF INVENTION: DETECTION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 07083, 000602
; CURRENT APPLICATION NUMBER: US/09/745,317
; CURRENT FILING DATE: 2000-12-21
```

```
;; PRIOR APPLICATION NUMBER: 60/173,268
;; PRIOR FILING DATE:
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 15
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:/No. US20020187470A1e =
US-09-745-317-15
```

```
Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      2 TGAGACCGATATCGGTC 20
        |||||
Db      23 TGCGCCCGAGATCGGTATC 5
```

```
RESULT 31
US-10-098-263B-130373
; Sequence 130373, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 130373
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-130373
```

```
Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      3 GAGACCGATATCGGTC 21
        |||||
Db      4 GAAACCGATATCGGTATCA 22
```

```
RESULT 32
US-10-098-263B-130373/c
; Sequence 130373, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 130373
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-130373
```

```
Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
```

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGTCTC 20
Db 22 TGATACCGATATCGTTTC 4

RESULT 33
US-10-098-263B-21859
; Sequence 21859, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-21859

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGATATCGGTCTCA 21
Db 11 CGATATCGGTCCCA 24

RESULT 34
US-10-098-263B-21859/c
; Sequence 21859, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-21859

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCG 15
Db 24 TGGAGCCGATATCG 11

RESULT 35
US-10-098-263B-30446
; Sequence 30446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30446

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 3 CTCTACCGAATTTGCTCAG 24

RESULT 36
US-10-098-263B-30446/c
; Sequence 30446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30446

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 24 CTGAGACCAATTTGCTAGAAG 3

RESULT 37
US-10-098-263B-70456
; Sequence 70456, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70456

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GATATCGGTCAG 22
|||||
Db 5 GATATCGGACTGAG 18

RESULT 38
US-10-098-263B-70456/c
; Sequence 70456, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70456

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATC 14
|||||
Db 18 CTGAGTCGATATC 5

RESULT 39
US-10-098-263B-87626
; Sequence 87626, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87626

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
|||||
Db 2 CTGATACCAATTGTGAGTCTCCG 23

RESULT 40
US-10-098-263B-87626/c
; Sequence 87626, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87626

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
|||||
Db 23 CGGAGACTCAATTGTGATCAG 2

Search completed: June 14, 2003, 23:29:10
Job time : 125 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 19:02:55 ; Search time 1368 Seconds
(without alignments)
260.454 Million cell updates/sec

Title: US-09-532-001-1

Perfect score: 22

Sequence: 1 CTGAGACCGATATCGTCTCAG 22

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*
1: em_estba:*
2: em_esthna:*
3: em_estnu:*
4: em_estnu:*
5: em_estnu:*
6: em_estnu:*
7: em_estnu:*
8: em_estnu:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est5:*
15: em_estfun:*
16: em_estfun:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.6	57.3	48	9	A1749566 ac30f01.x
2	12.6	57.3	48	9	A1749566 ac30f01.x
3	12.4	56.4	50	9	AU103408 AU103408
4	12.4	56.4	50	9	AU103408 AU103408
5	12	54.5	32	17	AZ511046 AU1035120
6	12	54.5	32	17	AZ511046 IM0355120

7	54.5	37	14	N32567	N32567 yw86e05.s1
8	54.5	37	14	N32567	N32567 yw86e05.s1
9	54.5	39	13	B1769009	B1769009 603058167
10	54.5	39	13	B1769009	B1769009 603058167
11	54.5	50	9	AU106749	AU106749 AU106749
12	54.5	50	9	AU106749	AU106749 AU106749
13	54.5	50	9	AU107183	AU107183 AU107183
14	54.5	50	9	AU107183	AU107183 AU107183
15	54.5	50	9	AU107184	AU107184 AU107184
16	54.5	50	9	AU107184	AU107184 AU107184
17	54.5	50	9	AU107185	AU107185 AU107185
18	54.5	50	9	AU107185	AU107185 AU107185
19	54.5	50	9	AU107188	AU107188 AU107188
20	54.5	50	9	AU107188	AU107188 AU107188
21	54.5	50	9	AU107189	AU107189 AU107189
22	54.5	50	9	AU107189	AU107189 AU107189
23	53.6	32	9	AU013431	AU013431 AU013431
24	53.6	32	9	AU013431	AU013431 AU013431
25	53.6	42	17	BH805089	BH805089 100806500
26	53.6	42	17	BH805089	BH805089 100806500
27	53.6	43	17	AZ304932	AZ304932 1M0005G03
28	53.6	43	17	AZ304932	AZ304932 1M0005G03
29	52.7	48	9	AU03871	AU03871 oc46c06.s
30	52.7	48	9	AU03871	AU03871 oc46c06.s
31	52.7	50	9	AU107186	AU107186 AU107186
32	52.7	50	9	AU107186	AU107186 AU107186
33	51.8	32	9	AU013455	AU013455 AU013455
34	51.8	32	9	AU013455	AU013455 AU013455
35	51.8	34	9	AU013784	AU013784 AU013784
36	51.8	34	9	AU013784	AU013784 AU013784
37	51.8	34	9	AU013851	AU013851 AU013851
38	51.8	34	9	AU013851	AU013851 AU013851
39	51.8	38	10	AV833036	AV833036 AV833036
40	51.8	38	10	AV833036	AV833036 AV833036
41	51.8	46	9	AU006689	AU006689 AU006689
42	51.8	46	9	AU006689	AU006689 AU006689
43	51.8	46	17	BH863926	BH863926 SALK_0949
44	51.8	46	17	BH863926	BH863926 SALK_0949
45	51.8	49	10	AM169662	AM169662 xj30606.x
46	51.8	49	10	AM169662	AM169662 xj30606.x
47	51.8	50	9	AU104209	AU104209 AU104209
48	51.8	50	9	AU104209	AU104209 AU104209
49	50.9	35	17	AZ591883	AZ591883 1M0402114
50	50.9	35	17	AZ591883	AZ591883 1M0402114
51	50.9	50	9	AU107997	AU107997 AU107997
52	50.9	50	9	AU107997	AU107997 AU107997
53	50.0	37	17	AZ806455	AZ806455 2M0068E04
54	50.0	37	17	AZ806455	AZ806455 2M0068E04
55	50.0	45	17	AZ810468	AZ810468 2M0076E02
56	50.0	45	17	AZ810468	AZ810468 2M0076E02
57	50.0	47	9	AU258690	AU258690 AU258690
58	50.0	47	9	AU258690	AU258690 AU258690
59	50.0	48	13	BM285362	BM285362 EST00003
60	50.0	48	13	BM285362	BM285362 EST00003
61	50.0	48	13	BM493234	BM493234 EST00017
62	50.0	48	13	BM493234	BM493234 EST00017
63	50.0	48	14	BO094078	BO094078 040802_37
64	50.0	48	14	BO094078	BO094078 040802_37
65	50.0	48	14	BO094080	BO094080 040802_39
66	50.0	48	14	BO094080	BO094080 040802_39
67	50.0	48	14	BO094081	BO094081 040802_40
68	50.0	48	14	BO094081	BO094081 040802_40
69	50.0	48	14	BO094082	BO094082 040802_41
70	50.0	48	14	BO094082	BO094082 040802_41
71	50.0	48	14	BO094086	BO094086 040802_45
72	50.0	48	14	BO094086	BO094086 040802_45
73	50.0	48	14	BO094088	BO094088 040802_47
74	50.0	48	14	BO094088	BO094088 040802_47
75	50.0	50	9	AU103727	AU103727 AU103727
76	50.0	50	9	AU103727	AU103727 AU103727
77	49.1	28	10	AM248289	AM248289 2819864.5
78	49.1	28	10	AM248289	AM248289 2819864.5
79	49.1	40	9	A1880105	A1880105 ap31d02.x

C 80	10.8	49.1	40	9	AI180105	AI180105	apj1d02.x	153	10	45.5	43	17	AZ830602	AZ830602	2M0109N24
C 81	10.8	49.1	40	17	AZ645161	AZ645161	IM0510N19	C 154	10	45.5	43	17	AZ830602	AZ830602	2M0109N24
C 82	10.8	49.1	40	17	AZ645161	AZ645161	IM0510N19	C 155	10	45.5	44	10	AV833060	AV833060	AV833060
C 83	10.8	49.1	43	9	AA932697	AA932697	co074d06.s	C 156	10	45.5	44	10	AV833060	AV833060	AV833060
C 84	10.8	49.1	43	9	AA932697	AA932697	co074d06.s	C 157	10	45.5	44	10	AV833060	AV833060	AV833060
C 85	10.8	49.1	43	9	AA974059	AA974059	co050h07.s	C 158	10	45.5	44	17	AZ509372	AZ509372	IM0352J17
C 86	10.8	49.1	43	9	AA974059	AA974059	co050h07.s	C 159	10	45.5	45	14	T17560	T17560	mps v16 The
C 87	10.8	49.1	44	13	BI860762	BI860762	603390194	C 160	10	45.5	45	14	T17560	T17560	mps v16 The
C 88	10.8	49.1	44	13	BI860762	BI860762	603390194	C 161	10	45.5	45	17	AZ465721	AZ465721	IM0275014
C 89	10.8	49.1	44	17	BH865755	BH865755	SALK_0998	C 162	10	45.5	45	17	AZ465721	AZ465721	IM0275014
C 90	10.8	49.1	44	17	BH865755	BH865755	SALK_0998	C 163	10	45.5	46	9	AA705006	AA705006	zj95e12.s
C 91	10.8	49.1	47	13	BI151478	BI151478	602917488	C 164	10	45.5	46	9	AA705006	AA705006	zj95e12.s
C 92	10.8	49.1	47	13	BI151478	BI151478	602917488	C 165	10	45.5	46	9	AU010025	AU010025	AU010025
C 93	10.8	49.1	50	9	AU104929	AU104929	AU104929	C 166	10	45.5	46	9	AU010025	AU010025	AU010025
C 94	10.8	49.1	50	9	AU104929	AU104929	AU104929	C 167	10	45.5	48	12	BF035895	BF035895	601457806
C 95	10.8	49.1	50	9	AU106987	AU106987	AU106987	C 168	10	45.5	48	12	BF035895	BF035895	601457806
C 96	10.8	49.1	50	9	AU106987	AU106987	AU106987	C 169	10	45.5	49	13	BI913160	BI913160	603179932
C 97	10.8	49.1	50	12	BG118504	BG118504	602348435	C 170	10	45.5	49	13	BI913160	BI913160	603179932
C 98	10.8	49.1	50	12	BG118504	BG118504	602348435	C 171	10	45.5	50	9	AU102324	AU102324	AU102324
C 99	10.8	49.1	50	12	BG178869	BG178869	602328026	C 172	10	45.5	50	9	AU102324	AU102324	AU102324
C 100	10.8	49.1	50	12	BG178869	BG178869	602328026	C 173	10	45.5	50	9	AU103849	AU103849	AU103849
C 101	10.6	48.2	22	17	AZ304010	AZ304010	IM0003023	C 174	10	45.5	50	9	AU103849	AU103849	AU103849
C 102	10.6	48.2	22	17	AZ304010	AZ304010	IM0003023	C 175	10	45.5	50	9	AU103849	AU103849	AU103849
C 103	10.6	48.2	28	17	BH864390	BH864390	SALK_0959	C 176	9.8	44.5	24	17	AZ367819	AZ367819	IM0117E05
C 104	10.6	48.2	28	17	BH864390	BH864390	SALK_0959	C 177	9.8	44.5	24	17	AZ367819	AZ367819	IM0117E05
C 105	10.6	48.2	38	17	BH864365	BH864365	SALK_0958	C 178	9.8	44.5	24	17	TA330F01Q	TA330F01Q	AL491983 T. brucei
C 106	10.6	48.2	38	17	BH864365	BH864365	SALK_0958	C 179	9.8	44.5	25	17	TA104C02Q	TA104C02Q	AL462285 T. brucei
C 107	10.6	48.2	44	17	AZ628166	AZ628166	IM0480C12	C 180	9.8	44.5	25	17	TA104C02Q	TA104C02Q	AL462285 T. brucei
C 108	10.6	48.2	44	17	AZ628166	AZ628166	IM0480C12	C 181	9.8	44.5	31	13	BI820240	BI820240	603037084
C 109	10.6	48.2	45	17	AZ828142	AZ828142	2M0104P24	C 182	9.8	44.5	31	13	BI820240	BI820240	603037084
C 110	10.6	48.2	45	17	AZ828142	AZ828142	2M0104P24	C 183	9.8	44.5	33	10	AV957156	AV957156	AV957156
C 111	10.6	48.2	50	9	AU104287	AU104287	AU104287	C 184	9.8	44.5	33	10	AV957156	AV957156	AV957156
C 112	10.6	48.2	50	9	AU104287	AU104287	AU104287	C 185	9.8	44.5	33	13	BM399063	BM399063	5009-0-52
C 113	10.4	47.3	32	13	BI739032	BI739032	603358882	C 186	9.8	44.5	33	13	BM399063	BM399063	5009-0-52
C 114	10.4	47.3	32	13	BI739032	BI739032	603358882	C 187	9.8	44.5	33	13	AZ352257	AZ352257	IM0090G11
C 115	10.4	47.3	35	17	AZ623458	AZ623458	IM0461D17	C 188	9.8	44.5	33	17	AZ352257	AZ352257	IM0090G11
C 116	10.4	47.3	35	17	AZ623458	AZ623458	IM0461D17	C 189	9.8	44.5	34	9	AA985167	AA985167	am79a09.s
C 117	10.4	47.3	36	9	AL646509	AL646509	AL646509	C 190	9.8	44.5	34	9	AA985167	AA985167	am79a09.s
C 118	10.4	47.3	36	9	AL646509	AL646509	AL646509	C 191	9.8	44.5	35	17	TA41H11P	TA41H11P	AL453757 T. brucei
C 119	10.4	47.3	50	9	AU103395	AU103395	AU103395	C 192	9.8	44.5	35	17	TA41H11P	TA41H11P	AL453757 T. brucei
C 120	10.4	47.3	50	9	AU103395	AU103395	AU103395	C 193	9.8	44.5	39	17	AZ773780	AZ773780	2M0001E02
C 121	10.4	47.3	50	9	AU104123	AU104123	AU104123	C 194	9.8	44.5	39	17	AZ773780	AZ773780	2M0001E02
C 122	10.4	47.3	50	9	AU104123	AU104123	AU104123	C 195	9.8	44.5	43	17	BH740846	BH740846	KG058224-3
C 123	10.4	47.3	50	9	AU104496	AU104496	AU104496	C 196	9.8	44.5	43	17	BH740846	BH740846	KG058224-3
C 124	10.4	47.3	50	9	AU104496	AU104496	AU104496	C 197	9.8	44.5	46	9	AI196701	AI196701	u153f07.y
C 125	10.2	46.4	43	9	AA011545	AA011545	z102d04.s	C 198	9.8	44.5	46	9	AI196701	AI196701	u153f07.y
C 126	10.2	46.4	43	9	AA011545	AA011545	z102d04.s	C 199	9.8	44.5	47	9	AA642360	AA642360	ns29f08.s
C 127	10.2	46.4	50	9	AU102352	AU102352	AU102352	C 200	9.8	44.5	47	9	AA642360	AA642360	ns29f08.s
C 128	10.2	46.4	50	9	AU102352	AU102352	AU102352	C 201	9.8	44.5	47	17	BH631605	BH631605	100708560
C 129	10.2	46.4	50	9	AU102353	AU102353	AU102353	C 202	9.8	44.5	47	17	BH631605	BH631605	100708560
C 130	10.2	46.4	50	9	AU102353	AU102353	AU102353	C 203	9.8	44.5	48	17	BH811778	BH811778	SALK_0601
C 131	10.2	46.4	50	9	AU102356	AU102356	AU102356	C 204	9.8	44.5	48	17	BH811778	BH811778	SALK_0601
C 132	10.2	46.4	50	9	AU102356	AU102356	AU102356	C 205	9.8	44.5	49	9	AI1004508	AI1004508	oc66g10.s
C 133	10.2	46.4	50	9	AU103419	AU103419	AU103419	C 206	9.8	44.5	49	9	AI1004508	AI1004508	oc66g10.s
C 134	10.2	46.4	50	9	AU103715	AU103715	AU103715	C 207	9.8	44.5	49	17	AL752628	AL752628	Arabiidops
C 135	10.2	46.4	50	9	AU103713	AU103713	AU103713	C 208	9.8	44.5	49	17	AL752628	AL752628	Arabiidops
C 136	10.2	46.4	50	9	AU103713	AU103713	AU103713	C 209	9.8	44.5	50	9	AU102274	AU102274	Arabiidops
C 137	10.2	46.4	50	9	AU103714	AU103714	AU103714	C 210	9.8	44.5	50	9	AU102274	AU102274	Arabiidops
C 138	10.2	46.4	50	9	AU103714	AU103714	AU103714	C 211	9.8	44.5	50	9	AU104024	AU104024	Arabiidops
C 139	10.2	46.4	50	9	AU103715	AU103715	AU103715	C 212	9.8	44.5	50	9	AU104024	AU104024	Arabiidops
C 140	10.2	46.4	50	9	AU103715	AU103715	AU103715	C 213	9.8	44.5	50	9	AU106341	AU106341	Arabiidops
C 141	10.2	46.4	50	9	AU107979	AU107979	AU107979	C 214	9.8	44.5	50	9	AU106341	AU106341	Arabiidops
C 142	10.2	46.4	50	9	AU107979	AU107979	AU107979	C 215	9.8	44.5	50	10	AM689710	AM689710	NF023E07S
C 143	10	45.5	28	17	AZ843789	AZ843789	2M0142L15	C 216	9.8	44.5	50	10	AM689710	AM689710	NF023E07S
C 144	10	45.5	28	17	AZ843789	AZ843789	2M0142L15	C 217	9.6	43.6	24	17	TA245F07P	TA245F07P	AL483592 T. brucei
C 145	10	45.5	33	17	TA69G09P	TA69G09P	AL457596 T. brucei	C 218	9.6	43.6	24	17	TA245F07P	TA245F07P	AL483592 T. brucei
C 146	10	45.5	33	17	TA69G09P	TA69G09P	AL457596 T. brucei	C 219	9.6	43.6	27	14	T17528	T17528	gstr m60 The
C 147	10	45.5	40	12	BG777922	BG777922	602665676	C 220	9.6	43.6	27	14	T17528	T17528	gstr m60 The
C 148	10	45.5	40	12	BG777922	BG777922	602665676	C 221	9.6	43.6	27	17	TA020H07P	TA020H07P	AL476110 T. brucei
C 149	10	45.5	40	12	BG778865	BG778865	602667554	C 222	9.6	43.6	27	17	TA020H07P	TA020H07P	AL476110 T. brucei
C 150	10	45.5	40	12	BG778865	BG778865	602667554	C 223	9.6	43.6	28	17	TA196E08Q	TA196E08Q	AL477877 T. brucei
C 151	10	45.5	40	17	AL756623	AL756623	Arabiidops	C 224	9.6	43.6	28	17	TA196E08Q	TA196E08Q	AL477877 T. brucei
C 152	10	45.5	40	17	AL756623	AL756623	Arabiidops	C 225	9.6	43.6	30	17	AZ786302	AZ786302	2M0031A13

C 226	9.6	43.6	30	17	AZ786302	2M0031A13	299	9.4	42.7	45	17	TA129F11P	AL464009 T. brucei
C 227	9.6	43.6	39	17	AL752652	Arabidops	C 300	9.4	42.7	46	17	TA129F11P	AL464009 T. brucei
C 228	9.6	43.6	39	17	AL752652	Arabidops	C 301	9.4	42.7	45	17	TA129F11P	AL464009 T. brucei
C 229	9.6	43.6	43	9	AA200880	mu03b12.r	C 302	9.4	42.7	46	9	AA064198	AA064198 mj62d12.r
C 230	9.6	43.6	43	9	AA200880	mu03b12.r	C 303	9.4	42.7	46	14	TA0386	TA0386 yd05d03.r1
C 231	9.6	43.6	46	14	N75232	N75232 yz73d12.r1	C 304	9.4	42.7	46	14	TA0386	TA0386 yd05d03.r1
C 232	9.6	43.6	48	14	N75232	N75232 yz73d12.r1	C 305	9.4	42.7	47	17	BH795957	BH795957 1008092B0
C 233	9.6	43.6	48	10	AV841288	AV841288	C 306	9.4	42.7	47	17	BH795957	BH795957 1008092B0
C 234	9.6	43.6	49	10	AV841288	AV841288	C 307	9.4	42.7	47	17	TA220G01P	AL480235 T. brucei
C 235	9.6	43.6	49	9	AI756242	AI756242	C 308	9.4	42.7	47	17	TA220G01P	AL480235 T. brucei
C 236	9.6	43.6	49	9	AI756242	AI756242	C 309	9.4	42.7	48	17	AZ830212	AZ830212 2M0109M16
C 237	9.6	43.6	49	13	BI518984	BI518984	C 310	9.4	42.7	48	17	AZ830212	AZ830212 2M0109M16
C 238	9.6	43.6	49	13	BI518984	BI518984	C 311	9.4	42.7	50	9	AU102347	AU102347 AU102347
C 239	9.6	43.6	50	9	AU104277	AU104277	C 312	9.4	42.7	50	9	AU102347	AU102347 AU102347
C 240	9.6	43.6	50	9	AU104277	AU104277	C 313	9.4	42.7	50	9	AU104211	AU104211 AU104211
C 241	9.6	43.6	50	9	AU106352	AU106352	C 314	9.4	42.7	50	9	AU104211	AU104211 AU104211
C 242	9.6	43.6	50	9	AU106352	AU106352	C 315	9.4	42.7	50	9	AU104352	AU104352 AU104352
C 243	9.6	43.6	50	9	AU107994	AU107994	C 316	9.4	42.7	50	9	AU104352	AU104352 AU104352
C 244	9.6	43.6	50	9	AU107994	AU107994	C 317	9.4	42.7	50	9	AU107136	AU107136 AU107136
C 245	9.4	42.7	25	14	L32057	L32057 HUMKPG6A H	C 318	9.4	42.7	50	9	AU107136	AU107136 AU107136
C 246	9.4	42.7	25	14	L32057	L32057 HUMKPG6A H	C 319	9.4	42.7	50	9	AU107137	AU107137 AU107137
C 247	9.4	42.7	29	9	AU012322	AU012322	C 320	9.4	42.7	50	9	AU107137	AU107137 AU107137
C 248	9.4	42.7	29	9	AU012322	AU012322	C 321	9.4	42.7	50	9	AU107139	AU107139 AU107139
C 249	9.4	42.7	30	9	AU012182	AU012182	C 322	9.4	42.7	50	9	AU107139	AU107139 AU107139
C 250	9.4	42.7	30	9	AU012182	AU012182	C 323	9.4	42.7	50	9	AU107140	AU107140 AU107140
C 251	9.4	42.7	30	9	AU256792	AU256792	C 324	9.4	42.7	50	9	AU107140	AU107140 AU107140
C 252	9.4	42.7	30	9	AU256792	AU256792	C 325	9.4	42.7	50	9	AU107141	AU107141 AU107141
C 253	9.4	42.7	31	17	AZ610795	AZ610795	C 326	9.4	42.7	50	9	AU107141	AU107141 AU107141
C 254	9.4	42.7	31	17	AZ610795	AZ610795	C 327	9.4	42.7	50	9	AU107142	AU107142 AU107142
C 255	9.4	42.7	31	17	AZ610795	AZ610795	C 328	9.4	42.7	50	9	AU107142	AU107142 AU107142
C 256	9.4	42.7	31	17	AZ610795	AZ610795	C 329	9.4	42.7	50	9	AU107187	AU107187 AU107187
C 257	9.4	42.7	32	17	TA13E07P	TA13E07P	C 330	9.4	42.7	50	9	AU107187	AU107187 AU107187
C 258	9.4	42.7	32	17	TA13E07P	TA13E07P	C 331	9.4	42.7	50	9	AU107626	AU107626 AU107626
C 259	9.4	42.7	34	9	AA436781	AA436781	C 332	9.4	42.7	50	9	AU107626	AU107626 AU107626
C 260	9.4	42.7	34	9	AA436781	AA436781	C 333	9.4	42.7	50	13	BI335418	BI335418 602998302
C 261	9.4	42.7	35	17	AZ428773	AZ428773	C 334	9.4	42.7	50	13	BI335418	BI335418 602998302
C 262	9.4	42.7	35	17	AZ428773	AZ428773	C 335	9.4	42.7	50	14	BQ789776	BQ789776 hage002A8
C 263	9.4	42.7	36	17	BH792341	BH792341	C 336	9.4	42.7	50	14	BQ789776	BQ789776 hage002A8
C 264	9.4	42.7	36	17	BH792341	BH792341	C 337	9.2	41.8	25	17	AZ655084	AZ655084 1M0529C30
C 265	9.4	42.7	37	9	AI120995	AI120995	C 338	9.2	41.8	25	17	AZ655084	AZ655084 1M0529C30
C 266	9.4	42.7	37	9	AI120995	AI120995	C 339	9.2	41.8	26	17	BH791427	BH791427 SALK_0599
C 267	9.4	42.7	37	9	AA275360	AA275360	C 340	9.2	41.8	26	17	BH791427	BH791427 SALK_0599
C 268	9.4	42.7	37	9	AA275360	AA275360	C 341	9.2	41.8	29	17	AZ683393	AZ683393 2M0171D04
C 269	9.4	42.7	38	9	AU259167	AU259167	C 342	9.2	41.8	29	17	AZ683393	AZ683393 2M0171D04
C 270	9.4	42.7	38	9	AU259167	AU259167	C 343	9.2	41.8	30	17	AL769095	AL769095 Arabidops
C 271	9.4	42.7	38	13	BJ015013	BJ015013	C 344	9.2	41.8	30	17	AL769095	AL769095 Arabidops
C 272	9.4	42.7	38	13	BJ015013	BJ015013	C 345	9.2	41.8	33	17	BH791695	BH791695 SALK_0608
C 273	9.4	42.7	39	9	AU011691	AU011691	C 346	9.2	41.8	33	17	TA210F03Q	TA210F03Q
C 274	9.4	42.7	39	9	AU011691	AU011691	C 347	9.2	41.8	34	17	TA210F03Q	TA210F03Q
C 275	9.4	42.7	39	17	AZ310708	AZ310708	C 348	9.2	41.8	35	17	AZ499700	AZ499700
C 276	9.4	42.7	39	17	AZ310708	AZ310708	C 349	9.2	41.8	35	17	AZ499700	AZ499700
C 277	9.4	42.7	40	9	AI570731	AI570731	C 350	9.2	41.8	35	17	AZ499700	AZ499700
C 278	9.4	42.7	40	9	AI570731	AI570731	C 351	9.2	41.8	36	12	BF159227	BF159227 601766682
C 279	9.4	42.7	40	9	AI761272	AI761272	C 352	9.2	41.8	36	12	BF159227	BF159227 601766682
C 280	9.4	42.7	40	9	AI761272	AI761272	C 353	9.2	41.8	36	17	AZ619194	AZ619194 1M0451J19
C 281	9.4	42.7	40	17	AZ772376	AZ772376	C 354	9.2	41.8	36	17	AZ619194	AZ619194 1M0451J19
C 282	9.4	42.7	40	17	AZ772376	AZ772376	C 355	9.2	41.8	36	17	BH812173	BH812173 SALK_0613
C 283	9.4	42.7	40	17	CNS07EUR	CNS07EUR	C 356	9.2	41.8	36	17	BH812173	BH812173 SALK_0613
C 284	9.4	42.7	40	17	CNS07EUR	CNS07EUR	C 357	9.2	41.8	37	10	AV847617	AV847617 AV847617
C 285	9.4	42.7	42	12	BG751431	BG751431	C 358	9.2	41.8	37	10	AV847617	AV847617 AV847617
C 286	9.4	42.7	42	12	BG751431	BG751431	C 359	9.2	41.8	38	17	AO025575	AO025575 fs(3)0564
C 287	9.4	42.7	42	17	AZ318518	AZ318518	C 360	9.2	41.8	38	17	AO025575	AO025575 fs(3)0564
C 288	9.4	42.7	42	17	AZ318518	AZ318518	C 361	9.2	41.8	40	9	AA588339	AA588339 tm93D07.s
C 289	9.4	42.7	42	17	AL762458	AL762458	C 362	9.2	41.8	40	9	AA588339	AA588339 tm93D07.s
C 290	9.4	42.7	42	17	AL762458	AL762458	C 363	9.2	41.8	40	17	DRE120T	DRE120T
C 291	9.4	42.7	43	9	AI098967	AI098967	C 364	9.2	41.8	40	17	DRE120T	DRE120T
C 292	9.4	42.7	43	9	AI098967	AI098967	C 365	9.2	41.8	41	13	BJ062022	BJ062022
C 293	9.4	42.7	43	17	AZ592609	AZ592609	C 366	9.2	41.8	41	13	BJ062022	BJ062022
C 294	9.4	42.7	43	17	AZ592609	AZ592609	C 367	9.2	41.8	41	17	BH863791	BH863791 SALK_0946
C 295	9.4	42.7	44	9	AU254864	AU254864	C 368	9.2	41.8	41	17	BH863791	BH863791 SALK_0946
C 296	9.4	42.7	44	9	AU254864	AU254864	C 369	9.2	41.8	42	10	AV833675	AV833675
C 297	9.4	42.7	44	13	BJ033903	BJ033903	C 370	9.2	41.8	42	10	AV833675	AV833675
C 298	9.4	42.7	44	13	BJ033903	BJ033903	C 371	9.2	41.8	43	9	AI152426	AI152426 ud91g05.r

C 372	9.2	41.8	43	9	AI152426	AI152426 udb905.r	445	9.2	41.8	50	9	AUI03140	AUI03140
C 373	9.2	41.8	44	14	R23375	R23375 yb33f01.s1	C 446	9.2	41.8	50	9	AUI03140	AUI03140
C 374	9.2	41.8	44	14	R23375	R23375 yb33f01.s1	C 447	9.2	41.8	50	9	AUI03141	AUI03141
C 375	9.2	41.8	44	17	AZ825920	AZ825920 2M0101C23	C 448	9.2	41.8	50	9	AUI03141	AUI03141
C 376	9.2	41.8	44	17	AZ825920	AZ825920 2M0101C23	C 449	9.2	41.8	50	9	AUI03142	AUI03142
C 377	9.2	41.8	44	17	BH862329	BH862329 SALK_0893	C 450	9.2	41.8	50	9	AUI03142	AUI03142
C 378	9.2	41.8	44	17	BH862329	BH862329 SALK_0893	C 451	9.2	41.8	50	9	AUI03144	AUI03144
C 379	9.2	41.8	45	17	AZ307664	AZ307664 1M0009J21	C 452	9.2	41.8	50	9	AUI03144	AUI03144
C 380	9.2	41.8	45	17	AZ307664	AZ307664 1M0009J21	C 453	9.2	41.8	50	9	AUI03145	AUI03145
C 381	9.2	41.8	45	17	BH812636	BH812636 SALK_0622	C 454	9.2	41.8	50	9	AUI03145	AUI03145
C 382	9.2	41.8	45	17	BH812636	BH812636 SALK_0622	C 455	9.2	41.8	50	9	AUI03146	AUI03146
C 383	9.2	41.8	46	14	R05843	R05843 yeb8e10.r1	C 456	9.2	41.8	50	9	AUI03146	AUI03146
C 384	9.2	41.8	46	14	R05843	R05843 yeb8e10.r1	C 457	9.2	41.8	50	9	AUI03245	AUI03245
C 385	9.2	41.8	46	14	R41260	R41260 yf85a04.s1	C 458	9.2	41.8	50	9	AUI03245	AUI03245
C 386	9.2	41.8	46	14	R41260	R41260 yf85a04.s1	C 459	9.2	41.8	50	9	AUI03969	AUI03969
C 387	9.2	41.8	46	17	AL769815	AL769815 Arabidops	C 460	9.2	41.8	50	9	AUI04155	AUI04155
C 388	9.2	41.8	46	17	AL769815	AL769815 Arabidops	C 461	9.2	41.8	50	9	AUI04155	AUI04155
C 389	9.2	41.8	46	17	AL769815	AL769815 Arabidops	C 462	9.2	41.8	50	9	AUI04155	AUI04155
C 390	9.2	41.8	48	13	BJ000382	BJ000382 BJ000382	C 463	9.2	41.8	50	9	AUI04252	AUI04252
C 391	9.2	41.8	48	13	BJ000382	BJ000382 BJ000382	C 464	9.2	41.8	50	9	AUI04252	AUI04252
C 392	9.2	41.8	49	9	AA789791	AA789791 vt79d11.r	C 465	9.2	41.8	50	9	AUI04254	AUI04254
C 393	9.2	41.8	49	9	AA789791	AA789791 vt79d11.r	C 466	9.2	41.8	50	9	AUI04254	AUI04254
C 394	9.2	41.8	50	9	AUI03108	AUI03108 AUI03108	C 467	9.2	41.8	50	9	AUI05016	AUI05016
C 395	9.2	41.8	50	9	AUI03109	AUI03109 AUI03109	C 468	9.2	41.8	50	9	AUI05016	AUI05016
C 396	9.2	41.8	50	9	AUI03109	AUI03109 AUI03109	C 469	9.2	41.8	50	9	AUI05082	AUI05082
C 397	9.2	41.8	50	9	AUI03110	AUI03110 AUI03110	C 470	9.2	41.8	50	9	AUI05082	AUI05082
C 398	9.2	41.8	50	9	AUI03110	AUI03110 AUI03110	C 471	9.2	41.8	50	9	AUI05212	AUI05212
C 399	9.2	41.8	50	9	AUI03111	AUI03111 AUI03111	C 472	9.2	41.8	50	9	AUI05472	AUI05472
C 400	9.2	41.8	50	9	AUI03111	AUI03111 AUI03111	C 473	9.2	41.8	50	9	AUI05472	AUI05472
C 401	9.2	41.8	50	9	AUI03113	AUI03113 AUI03113	C 474	9.2	41.8	50	9	AUI05473	AUI05473
C 402	9.2	41.8	50	9	AUI03113	AUI03113 AUI03113	C 475	9.2	41.8	50	9	AUI05473	AUI05473
C 403	9.2	41.8	50	9	AUI03114	AUI03114 AUI03114	C 476	9.2	41.8	50	9	AUI05474	AUI05474
C 404	9.2	41.8	50	9	AUI03115	AUI03115 AUI03115	C 477	9.2	41.8	50	9	AUI05474	AUI05474
C 405	9.2	41.8	50	9	AUI03115	AUI03115 AUI03115	C 478	9.2	41.8	50	9	AUI05475	AUI05475
C 406	9.2	41.8	50	9	AUI03115	AUI03115 AUI03115	C 479	9.2	41.8	50	9	AUI05475	AUI05475
C 407	9.2	41.8	50	9	AUI03116	AUI03116 AUI03116	C 480	9.2	41.8	50	9	AUI05476	AUI05476
C 408	9.2	41.8	50	9	AUI03116	AUI03116 AUI03116	C 481	9.2	41.8	50	9	AUI05476	AUI05476
C 409	9.2	41.8	50	9	AUI03117	AUI03117 AUI03117	C 482	9.2	41.8	50	9	AUI05479	AUI05479
C 410	9.2	41.8	50	9	AUI03117	AUI03117 AUI03117	C 483	9.2	41.8	50	9	AUI05479	AUI05479
C 411	9.2	41.8	50	9	AUI03118	AUI03118 AUI03118	C 484	9.2	41.8	50	9	AUI05480	AUI05480
C 412	9.2	41.8	50	9	AUI03118	AUI03118 AUI03118	C 485	9.2	41.8	50	9	AUI05480	AUI05480
C 413	9.2	41.8	50	9	AUI03119	AUI03119 AUI03119	C 486	9.2	41.8	50	9	AUI05480	AUI05480
C 414	9.2	41.8	50	9	AUI03119	AUI03119 AUI03119	C 487	9.2	41.8	50	9	AUI05862	AUI05862
C 415	9.2	41.8	50	9	AUI03121	AUI03121 AUI03121	C 488	9.2	41.8	50	9	AUI05862	AUI05862
C 416	9.2	41.8	50	9	AUI03121	AUI03121 AUI03121	C 489	9.2	41.8	50	9	AUI06400	AUI06400
C 417	9.2	41.8	50	9	AUI03121	AUI03121 AUI03121	C 490	9.2	41.8	50	9	AUI06400	AUI06400
C 418	9.2	41.8	50	9	AUI03123	AUI03123 AUI03123	C 491	9.2	41.8	50	9	AUI06401	AUI06401
C 419	9.2	41.8	50	9	AUI03124	AUI03124 AUI03124	C 492	9.2	41.8	50	9	AUI06401	AUI06401
C 420	9.2	41.8	50	9	AUI03124	AUI03124 AUI03124	C 493	9.2	41.8	50	9	AUI06403	AUI06403
C 421	9.2	41.8	50	9	AUI03125	AUI03125 AUI03125	C 494	9.2	41.8	50	9	AUI06403	AUI06403
C 422	9.2	41.8	50	9	AUI03125	AUI03125 AUI03125	C 495	9.2	41.8	50	9	AUI06404	AUI06404
C 423	9.2	41.8	50	9	AUI03127	AUI03127 AUI03127	C 496	9.2	41.8	50	9	AUI06404	AUI06404
C 424	9.2	41.8	50	9	AUI03127	AUI03127 AUI03127	C 497	9.2	41.8	50	9	AUI06408	AUI06408
C 425	9.2	41.8	50	9	AUI03128	AUI03128 AUI03128	C 498	9.2	41.8	50	9	AUI06408	AUI06408
C 426	9.2	41.8	50	9	AUI03128	AUI03128 AUI03128	C 499	9.2	41.8	50	9	AUI06409	AUI06409
C 427	9.2	41.8	50	9	AUI03129	AUI03129 AUI03129	C 500	9.2	41.8	50	9	AUI06409	AUI06409
C 428	9.2	41.8	50	9	AUI03129	AUI03129 AUI03129	C 501	9.2	41.8	50	9	AUI06410	AUI06410
C 429	9.2	41.8	50	9	AUI03130	AUI03130 AUI03130	C 502	9.2	41.8	50	9	AUI06410	AUI06410
C 430	9.2	41.8	50	9	AUI03130	AUI03130 AUI03130	C 503	9.2	41.8	50	9	AUI06412	AUI06412
C 431	9.2	41.8	50	9	AUI03131	AUI03131 AUI03131	C 504	9.2	41.8	50	9	AUI06412	AUI06412
C 432	9.2	41.8	50	9	AUI03131	AUI03131 AUI03131	C 505	9.2	41.8	50	9	AUI06419	AUI06419
C 433	9.2	41.8	50	9	AUI03132	AUI03132 AUI03132	C 506	9.2	41.8	50	9	AUI06419	AUI06419
C 434	9.2	41.8	50	9	AUI03132	AUI03132 AUI03132	C 507	9.2	41.8	50	9	AUI06421	AUI06421
C 435	9.2	41.8	50	9	AUI03133	AUI03133 AUI03133	C 508	9.2	41.8	50	9	AUI06421	AUI06421
C 436	9.2	41.8	50	9	AUI03133	AUI03133 AUI03133	C 509	9.2	41.8	50	9	AUI06425	AUI06425
C 437	9.2	41.8	50	9	AUI03134	AUI03134 AUI03134	C 510	9.2	41.8	50	9	AUI06425	AUI06425
C 438	9.2	41.8	50	9	AUI03134	AUI03134 AUI03134	C 511	9.2	41.8	50	9	AUI06430	AUI06430
C 439	9.2	41.8	50	9	AUI03135	AUI03135 AUI03135	C 512	9.2	41.8	50	9	AUI06430	AUI06430
C 440	9.2	41.8	50	9	AUI03135	AUI03135 AUI03135	C 513	9.2	41.8	50	9	AUI06432	AUI06432
C 441	9.2	41.8	50	9	AUI03138	AUI03138 AUI03138	C 514	9.2	41.8	50	9	AUI06432	AUI06432
C 442	9.2	41.8	50	9	AUI03138	AUI03138 AUI03138	C 515	9.2	41.8	50	9	AUI06433	AUI06433
C 443	9.2	41.8	50	9	AUI03139	AUI03139 AUI03139	C 516	9.2	41.8	50	9	AUI06433	AUI06433
C 444	9.2	41.8	50	9	AUI03139	AUI03139 AUI03139	C 517	9.2	41.8	50	9	AUI06435	AUI06435

C 518	9.2	41.8	50	9	AUI06435	AUI06435	AUI06435	591	9	40.9	32	17	TA60B12Q	AL455905 T. brucei
C 519	9.2	41.8	50	9	AUI06438	AUI06438	AUI06438	C 592	9	40.9	32	17	TA60B12Q	AL455905 T. brucei
C 520	9.2	41.8	50	9	AUI06438	AUI06438	AUI06438	C 593	9	40.9	34	17	TA60B12Q	AL455905 T. brucei
C 521	9.2	41.8	50	9	AUI06442	AUI06442	AUI06442	C 594	9	40.9	32	17	TA60B12Q	AL455905 T. brucei
C 522	9.2	41.8	50	9	AUI06442	AUI06442	AUI06442	C 595	9	40.9	34	17	TA60B12Q	AL455905 T. brucei
C 523	9.2	41.8	50	9	AUI06444	AUI06444	AUI06444	C 596	9	40.9	34	17	TA60B12Q	AL455905 T. brucei
C 524	9.2	41.8	50	9	AUI06444	AUI06444	AUI06444	C 597	9	40.9	34	17	TA60B12Q	AL455905 T. brucei
C 525	9.2	41.8	50	9	AUI06446	AUI06446	AUI06446	C 598	9	40.9	36	17	TA100G04Q	AL459362 T. brucei
C 526	9.2	41.8	50	9	AUI06446	AUI06446	AUI06446	C 599	9	40.9	36	17	TA100G04Q	AL459362 T. brucei
C 527	9.2	41.8	50	9	AUI06449	AUI06449	AUI06449	C 600	9	40.9	37	9	AL677081	AL677081
C 528	9.2	41.8	50	9	AUI06449	AUI06449	AUI06449	C 601	9	40.9	37	17	AL753259	AL753259
C 529	9.2	41.8	50	9	AUI06452	AUI06452	AUI06452	C 602	9	40.9	37	17	AL753259	AL753259
C 530	9.2	41.8	50	9	AUI06452	AUI06452	AUI06452	C 603	9	40.9	38	17	AL753259	AL753259
C 531	9.2	41.8	50	9	AUI06459	AUI06459	AUI06459	C 604	9	40.9	38	17	AL753259	AL753259
C 532	9.2	41.8	50	9	AUI06459	AUI06459	AUI06459	C 605	9	40.9	38	17	AL753259	AL753259
C 533	9.2	41.8	50	9	AUI06460	AUI06460	AUI06460	C 606	9	40.9	39	10	BE544028	BE544028
C 534	9.2	41.8	50	9	AUI06460	AUI06460	AUI06460	C 607	9	40.9	39	10	BE544028	BE544028
C 535	9.2	41.8	50	9	AUI06467	AUI06467	AUI06467	C 608	9	40.9	40	9	AI366718	AI366718
C 536	9.2	41.8	50	9	AUI06467	AUI06467	AUI06467	C 609	9	40.9	40	9	AI366718	AI366718
C 537	9.2	41.8	50	9	AUI06498	AUI06498	AUI06498	C 610	9	40.9	40	9	AA237539	AA237539
C 538	9.2	41.8	50	9	AUI06498	AUI06498	AUI06498	C 611	9	40.9	40	9	AA237539	AA237539
C 539	9.2	41.8	50	9	AUI06499	AUI06499	AUI06499	C 612	9	40.9	40	13	BU066312	BU066312
C 540	9.2	41.8	50	9	AUI06499	AUI06499	AUI06499	C 613	9	40.9	40	13	BU066312	BU066312
C 541	9.2	41.8	50	9	AUI06504	AUI06504	AUI06504	C 614	9	40.9	40	17	AL753351	AL753351
C 542	9.2	41.8	50	9	AUI06504	AUI06504	AUI06504	C 615	9	40.9	41	12	BC472622	BC472622
C 543	9.2	41.8	50	9	AUI06505	AUI06505	AUI06505	C 616	9	40.9	41	12	BC472622	BC472622
C 544	9.2	41.8	50	9	AUI06505	AUI06505	AUI06505	C 617	9	40.9	42	17	AZ472668	AZ472668
C 545	9.2	41.8	50	9	AUI06507	AUI06507	AUI06507	C 618	9	40.9	42	17	AZ472668	AZ472668
C 546	9.2	41.8	50	9	AUI06507	AUI06507	AUI06507	C 619	9	40.9	43	17	BH891787	BH891787
C 547	9.2	41.8	50	9	AUI06508	AUI06508	AUI06508	C 620	9	40.9	43	17	BH891787	BH891787
C 548	9.2	41.8	50	9	AUI06510	AUI06510	AUI06510	C 621	9	40.9	44	17	AQ025716	AQ025716
C 549	9.2	41.8	50	9	AUI06510	AUI06510	AUI06510	C 622	9	40.9	44	17	AQ025716	AQ025716
C 550	9.2	41.8	50	9	AUI06511	AUI06511	AUI06511	C 623	9	40.9	45	14	H67715	H67715
C 551	9.2	41.8	50	9	AUI06511	AUI06511	AUI06511	C 624	9	40.9	45	14	H67715	H67715
C 552	9.2	41.8	50	9	AUI06511	AUI06511	AUI06511	C 625	9	40.9	46	17	TA212P10Q	TA212P10Q
C 553	9.2	41.8	50	9	AUI06514	AUI06514	AUI06514	C 626	9	40.9	46	17	TA212P10Q	TA212P10Q
C 554	9.2	41.8	50	9	AUI06514	AUI06514	AUI06514	C 627	9	40.9	48	17	AZ602280	AZ602280
C 555	9.2	41.8	50	9	AUI06526	AUI06526	AUI06526	C 628	9	40.9	48	17	AZ602280	AZ602280
C 556	9.2	41.8	50	9	AUI06526	AUI06526	AUI06526	C 629	9	40.9	49	12	BF034811	BF034811
C 557	9.2	41.8	50	9	AUI06527	AUI06527	AUI06527	C 630	9	40.9	49	12	BF034811	BF034811
C 558	9.2	41.8	50	9	AUI06528	AUI06528	AUI06528	C 631	9	40.9	49	17	BH803126	BH803126
C 559	9.2	41.8	50	9	AUI06528	AUI06528	AUI06528	C 632	9	40.9	49	17	BH803126	BH803126
C 560	9.2	41.8	50	9	AUI06530	AUI06530	AUI06530	C 633	9	40.9	49	17	BH855856	BH855856
C 561	9.2	41.8	50	9	AUI06530	AUI06530	AUI06530	C 634	9	40.9	49	17	BH855856	BH855856
C 562	9.2	41.8	50	9	AUI06531	AUI06531	AUI06531	C 635	9	40.9	49	17	BH855857	BH855857
C 563	9.2	41.8	50	9	AUI06531	AUI06531	AUI06531	C 636	9	40.9	49	17	BH855857	BH855857
C 564	9.2	41.8	50	9	AUI06532	AUI06532	AUI06532	C 637	9	40.9	50	9	AUI02673	AUI02673
C 565	9.2	41.8	50	9	AUI06532	AUI06532	AUI06532	C 638	9	40.9	50	9	AUI02673	AUI02673
C 566	9.2	41.8	50	9	AUI06533	AUI06533	AUI06533	C 639	9	40.9	50	9	AUI03412	AUI03412
C 567	9.2	41.8	50	9	AUI06533	AUI06533	AUI06533	C 640	9	40.9	50	9	AUI03412	AUI03412
C 568	9.2	41.8	50	9	AUI06533	AUI06533	AUI06533	C 641	9	40.9	50	9	AUI03412	AUI03412
C 569	9.2	41.8	50	9	AUI06534	AUI06534	AUI06534	C 642	9	40.9	50	9	AUI03412	AUI03412
C 570	9.2	41.8	50	9	AUI06534	AUI06534	AUI06534	C 643	9	40.9	50	9	AUI03412	AUI03412
C 571	9.2	41.8	50	9	AUI06536	AUI06536	AUI06536	C 644	9	40.9	50	9	AUI03925	AUI03925
C 572	9.2	41.8	50	9	AUI06536	AUI06536	AUI06536	C 645	9	40.9	50	9	AUI03925	AUI03925
C 573	9.2	41.8	50	9	AUI06537	AUI06537	AUI06537	C 646	9	40.9	50	9	AUI03979	AUI03979
C 574	9.2	41.8	50	9	AUI06537	AUI06537	AUI06537	C 647	9	40.9	50	9	AUI03979	AUI03979
C 575	9.2	41.8	50	9	AUI06539	AUI06539	AUI06539	C 648	9	40.9	50	9	AUI04912	AUI04912
C 576	9.2	41.8	50	9	AUI06539	AUI06539	AUI06539	C 649	9	40.9	50	9	AUI04912	AUI04912
C 577	9.2	41.8	50	9	AUI06543	AUI06543	AUI06543	C 650	9	40.9	50	9	AUI07941	AUI07941
C 578	9.2	41.8	50	9	AUI06543	AUI06543	AUI06543	C 651	9	40.9	50	9	AA430812	AA430812
C 579	9.2	41.8	50	9	AUI07046	AUI07046	AUI07046	C 652	9	40.9	50	9	AA430812	AA430812
C 580	9.2	41.8	50	9	AUI07046	AUI07046	AUI07046	C 653	9	40.9	50	17	AZ820525	AZ820525
C 581	9.2	41.8	50	9	BM393606	BM393606	BM393606	C 654	9	40.9	50	17	AZ820525	AZ820525
C 582	9.2	41.8	50	9	BM393606	BM393606	BM393606	C 655	9	40.9	50	17	AZ820525	AZ820525
C 583	9.2	41.8	50	9	AZ810962	AZ810962	AZ810962	C 656	9	40.9	50	17	TA374G11Q	TA374G11Q
C 584	9.2	41.8	50	9	AZ810962	AZ810962	AZ810962	C 657	9	40.9	50	17	TA374G11Q	TA374G11Q
C 585	9.2	41.8	50	9	BH861244	BH861244	BH861244	C 658	9	40.9	17	13	BM398854	BM398854
C 586	9.2	41.8	50	9	BH861244	BH861244	BH861244	C 659	9	40.9	17	13	BM398854	BM398854
C 587	9.2	41.8	50	9	BH861245	BH861245	BH861245	C 660	9	40.9	25	10	AM246508	AM246508
C 588	9.2	41.8	50	9	BH861245	BH861245	BH861245	C 661	9	40.9	25	10	AM246508	AM246508
C 589	9.2	41.8	50	9	AI493525	AI493525	AI493525	C 662	9	40.9	25	17	AZ464201	AZ464201
C 590	9.2	41.8	50	9	AI493525	AI493525	AI493525	C 663	9	40.9	25	17	TA132G12P	TA132G12P

C 664	8.8	40.0	25	17	TA132G12P	AL465564 T. brucei	737	8.8	40.0	43	9	A1789878	A1789878 ue65f10.r
C 665	8.8	40.0	27	2	HSM007348	A1042498 Homo sapi	C 738	8.8	40.0	43	9	A1789878	A1789878 ue65f10.r
C 666	8.8	40.0	27	2	HSM007348	A1042498 Homo sapi	C 739	8.8	40.0	43	10	AM064197	AM064197 SP0644 KR
C 667	8.8	40.0	28	2	HSM007350	A1042500 Homo sapi	C 740	8.8	40.0	43	10	AM064197	AM064197 SP0644 KR
C 668	8.8	40.0	28	2	HSM007350	A1042500 Homo sapi	C 741	8.8	40.0	43	14	C00370	C00370 HUMGS000366
C 669	8.8	40.0	29	17	AZ966795	AZ966795 2M0237P23	C 742	8.8	40.0	43	14	C00370	C00370 HUMGS000366
C 670	8.8	40.0	29	17	AZ966795	AZ966795 2M0237P23	C 743	8.8	40.0	43	17	AZ305746	AZ305746 1M0006J06
C 671	8.8	40.0	31	17	BH791422	BH791422 SALK_0599	C 744	8.8	40.0	43	17	AZ305746	AZ305746 1M0006J06
C 672	8.8	40.0	31	17	BH791422	BH791422 SALK_0599	C 745	8.8	40.0	43	17	AZ305746	AZ305746 1M0006J06
C 673	8.8	40.0	32	17	AL754213	AL754213 Arabidops	C 746	8.8	40.0	43	17	AZ575514	AZ575514 AST-T21F0
C 674	8.8	40.0	32	17	AL754213	AL754213 Arabidops	C 747	8.8	40.0	43	17	AZ575514	AZ575514 AST-T21F0
C 675	8.8	40.0	33	17	AZ458451	AZ458451 1M0262L01	C 748	8.8	40.0	43	17	AZ784062	AZ784062 2M0026M21
C 676	8.8	40.0	33	17	AZ458451	AZ458451 1M0262L01	C 749	8.8	40.0	43	17	AZ784062	AZ784062 2M0026M21
C 677	8.8	40.0	34	9	AA988881	AA988881 or86d09.s	C 750	8.8	40.0	43	17	AZ842357	AZ842357 2M0140J16
C 678	8.8	40.0	34	9	AA988881	AA988881 or86d09.s	C 751	8.8	40.0	43	17	AZ842357	AZ842357 2M0140J16
C 679	8.8	40.0	34	12	BF576427	BF576427 602133840	C 752	8.8	40.0	43	17	BH892666	BH892666 3526_1_22
C 680	8.8	40.0	34	12	BF576427	BF576427 602133840	C 753	8.8	40.0	44	12	BG779515	BG779515 602666932
C 681	8.8	40.0	35	9	AU244156	AU244156 AU244156	C 754	8.8	40.0	44	12	BG779515	BG779515 602666932
C 682	8.8	40.0	35	9	AU244156	AU244156 AU244156	C 755	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 683	8.8	40.0	35	12	BG529663	BG529663 602558102	C 756	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 684	8.8	40.0	35	12	BG529663	BG529663 602558102	C 757	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 685	8.8	40.0	36	12	BF790288	BF790288 602249513	C 758	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 686	8.8	40.0	36	12	BF790288	BF790288 602249513	C 759	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 687	8.8	40.0	36	14	C00778	C00778 HUMGS000239	C 760	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 688	8.8	40.0	36	14	C00778	C00778 HUMGS000239	C 761	8.8	40.0	45	10	AV844706	AV844706 AV844706
C 689	8.8	40.0	36	14	H45291	H45291 yn99d02.s1	C 762	8.8	40.0	45	10	AV844706	AV844706 AV844706
C 690	8.8	40.0	36	14	H45291	H45291 yn99d02.s1	C 763	8.8	40.0	45	13	B1067044	B1067044 B1067044
C 691	8.8	40.0	36	17	BH789699	BH789699 SALK_0444	C 764	8.8	40.0	45	13	B1067044	B1067044 B1067044
C 692	8.8	40.0	36	17	BH789699	BH789699 SALK_0444	C 765	8.8	40.0	45	14	D45793	D45793 HUMGS03008
C 693	8.8	40.0	36	17	BH857872	BH857872 SALK_0875	C 766	8.8	40.0	45	14	D45793	D45793 HUMGS03008
C 694	8.8	40.0	36	17	BH857872	BH857872 SALK_0875	C 767	8.8	40.0	45	17	AZ432380	AZ432380 1M0217H13
C 695	8.8	40.0	37	9	AA681821	AA681821 v065h03.r	C 768	8.8	40.0	45	17	AZ432380	AZ432380 1M0217H13
C 696	8.8	40.0	37	9	AA681821	AA681821 v065h03.r	C 769	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 697	8.8	40.0	37	9	AA681821	AA681821 v065h03.r	C 770	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 698	8.8	40.0	37	9	AA135712	AA135712 qv17h02.x	C 771	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 699	8.8	40.0	37	9	AA112840	AA112840 zns4f01.r	C 772	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 700	8.8	40.0	37	9	AA112840	AA112840 zns4f01.r	C 773	8.8	40.0	46	17	BH759240	BH759240 KG00542-3
C 701	8.8	40.0	37	17	AZ814152	AZ814152 2M0081C13	C 774	8.8	40.0	46	9	AA837899	AA837899 1008110H1
C 702	8.8	40.0	37	17	AZ814152	AZ814152 2M0081C13	C 775	8.8	40.0	46	9	AA837899	AA837899 1008110H1
C 703	8.8	40.0	37	17	BH809857	BH809857 SALK_0064	C 776	8.8	40.0	46	9	AA837899	AA837899 1008110H1
C 704	8.8	40.0	37	17	BH809857	BH809857 SALK_0064	C 777	8.8	40.0	46	9	AA837899	AA837899 1008110H1
C 705	8.8	40.0	38	17	AZ439902	AZ439902 1M0230C13	C 778	8.8	40.0	46	9	AA837899	AA837899 1008110H1
C 706	8.8	40.0	38	17	AZ439902	AZ439902 1M0230C13	C 779	8.8	40.0	46	9	AA837899	AA837899 1008110H1
C 707	8.8	40.0	38	17	AZ772664	AZ772664 1M0583B16	C 780	8.8	40.0	46	14	D26039	D26039 HUMGS03662
C 708	8.8	40.0	38	17	AZ772664	AZ772664 1M0583B16	C 781	8.8	40.0	46	14	D26039	D26039 HUMGS03662
C 709	8.8	40.0	39	10	AV833438	AV833438 AV833438	C 782	8.8	40.0	46	14	D26039	D26039 HUMGS03662
C 710	8.8	40.0	39	10	AV833438	AV833438 AV833438	C 783	8.8	40.0	46	14	D26039	D26039 HUMGS03662
C 711	8.8	40.0	39	10	BE617821	BE617821 601441869	C 784	8.8	40.0	47	12	BG484978	BG484978 602503986
C 712	8.8	40.0	39	10	BE617821	BE617821 601441869	C 785	8.8	40.0	47	12	BG484978	BG484978 602503986
C 713	8.8	40.0	39	12	BF028281	BF028281 601765059	C 786	8.8	40.0	47	17	AZ476231	AZ476231 1M0294P14
C 714	8.8	40.0	39	12	BF028281	BF028281 601765059	C 787	8.8	40.0	47	17	AZ476231	AZ476231 1M0294P14
C 715	8.8	40.0	39	14	D26027	D26027 HUMGS02394	C 788	8.8	40.0	47	17	AZ476231	AZ476231 1M0294P14
C 716	8.8	40.0	39	14	D26027	D26027 HUMGS02394	C 789	8.8	40.0	47	17	AZ476231	AZ476231 1M0294P14
C 717	8.8	40.0	39	17	BH811645	BH811645 SALK_0595	C 790	8.8	40.0	47	17	BH636648	BH636648 1008012E0
C 718	8.8	40.0	39	17	BH811645	BH811645 SALK_0595	C 791	8.8	40.0	47	17	BH636648	BH636648 1008012E0
C 719	8.8	40.0	39	17	TA268H08Q	TA268H08Q	C 792	8.8	40.0	47	17	BH636648	BH636648 1008012E0
C 720	8.8	40.0	39	17	TA268H08Q	TA268H08Q	C 793	8.8	40.0	48	17	BH636648	BH636648 1008012E0
C 721	8.8	40.0	40	9	A1123628	A1123628 co15h04.x	C 794	8.8	40.0	48	17	BH636648	BH636648 1008012E0
C 722	8.8	40.0	40	9	A1123628	A1123628 co15h04.x	C 795	8.8	40.0	49	9	A1808123	A1808123 w553d07.x
C 723	8.8	40.0	40	9	AA529801	AA529801 vj12d07.r	C 796	8.8	40.0	49	9	A1808123	A1808123 w553d07.x
C 724	8.8	40.0	40	9	AA529801	AA529801 vj12d07.r	C 797	8.8	40.0	49	9	A1808123	A1808123 w553d07.x
C 725	8.8	40.0	42	9	AL677123	AL677123 AL677123	C 798	8.8	40.0	49	17	BH130349	BH130349 G-6P13.F
C 726	8.8	40.0	42	9	AL677123	AL677123 AL677123	C 799	8.8	40.0	50	9	BH130349	BH130349 G-6P13.F
C 727	8.8	40.0	42	17	AZ777273	AZ777273 2M0011M04	C 800	8.8	40.0	50	9	AU102628	AU102628 AU102628
C 728	8.8	40.0	42	17	AZ777273	AZ777273 2M0011M04	C 801	8.8	40.0	50	9	AU102628	AU102628 AU102628
C 729	8.8	40.0	42	17	AZ805941	AZ805941 2M0067B07	C 802	8.8	40.0	50	9	AU102628	AU102628 AU102628
C 730	8.8	40.0	42	17	AZ805941	AZ805941 2M0067B07	C 803	8.8	40.0	50	9	AU102628	AU102628 AU102628
C 731	8.8	40.0	42	17	AZ867147	AZ867147 2M0177E21	C 804	8.8	40.0	50	9	AU103136	AU103136 AU103136
C 732	8.8	40.0	42	17	AZ867147	AZ867147 2M0177E21	C 805	8.8	40.0	50	9	AU103136	AU103136 AU103136
C 733	8.8	40.0	42	17	AL757728	AL757728 Arabidops	C 806	8.8	40.0	50	9	AU103136	AU103136 AU103136
C 734	8.8	40.0	43	17	AL757728	AL757728 Arabidops	C 807	8.8	40.0	50	9	AU103136	AU103136 AU103136
C 735	8.8	40.0	43	17	AA878868	AA878868 cf88e01.s	C 808	8.8	40.0	50	9	AU103136	AU103136 AU103136
C 736	8.8	40.0	43	9	AA878868	AA878868 cf88e01.s	C 809	8.8	40.0	50	9	AU103136	AU103136 AU103136

C 810	8.8	40.0	50	9	AU103143	AU103143	AU103143	883	8.6	39.1	36	17	AL771940	AL771940 Arabidops
C 811	8.8	40.0	50	9	AU103148	AU103148	AU103148	C 884	8.6	39.1	36	17	AL771940	AL771940 Arabidops
C 812	8.8	40.0	50	9	AU103148	AU103148	AU103148	C 885	39.1	36	17	TA345F06Q	TA345F06Q T. brucei	
C 813	8.8	40.0	50	9	AU103150	AU103150	AU103150	C 886	8.6	39.1	36	17	TA345F06Q	TA345F06Q T. brucei
C 814	8.8	40.0	50	9	AU103150	AU103150	AU103150	C 887	39.1	36	17	TA345F06Q	TA345F06Q T. brucei	
C 815	8.8	40.0	50	9	AU103828	AU103828	AU103828	C 888	8.6	39.1	37	9	AA007962	AA007962 mg66907.r
C 816	8.8	40.0	50	9	AU103828	AU103828	AU103828	C 889	8.6	39.1	37	9	AA007962	AA007962 mg66907.r
C 817	8.8	40.0	50	9	AU104007	AU104007	AU104007	C 890	8.6	39.1	37	9	AA889248	AA889248 ak26d11.s
C 818	8.8	40.0	50	9	AU104007	AU104007	AU104007	C 891	8.6	39.1	37	9	AA889248	AA889248 ak26d11.s
C 819	8.8	40.0	50	9	AU104105	AU104105	AU104105	C 892	8.6	39.1	37	17	AZ593655	AZ593655 1M040516
C 820	8.8	40.0	50	9	AU104105	AU104105	AU104105	C 893	8.6	39.1	37	17	AZ593655	AZ593655 1M040516
C 821	8.8	40.0	50	9	AU104120	AU104120	AU104120	C 894	8.6	39.1	37	17	AZ776442	AZ776442 2M0010L02
C 822	8.8	40.0	50	9	AU104120	AU104120	AU104120	C 895	8.6	39.1	37	17	AZ776442	AZ776442 2M0010L02
C 823	8.8	40.0	50	9	AU104350	AU104350	AU104350	C 896	8.6	39.1	37	17	AZ806718	AZ806718 2M0068024
C 824	8.8	40.0	50	9	AU104350	AU104350	AU104350	C 897	8.6	39.1	37	17	TA126E11P	AZ806718 2M0068024
C 825	8.8	40.0	50	9	AU104585	AU104585	AU104585	C 898	8.6	39.1	37	17	TA126E11P	AL463841 T. brucei
C 826	8.8	40.0	50	9	AU104585	AU104585	AU104585	C 899	8.6	39.1	38	12	BF137365	AL463841 T. brucei
C 827	8.8	40.0	50	9	AU104586	AU104586	AU104586	C 900	8.6	39.1	38	12	BF137365	BF137365 601780736
C 828	8.8	40.0	50	9	AU104586	AU104586	AU104586	C 901	8.6	39.1	38	13	BF137365	BF137365 601780736
C 829	8.8	40.0	50	9	AU104589	AU104589	AU104589	C 902	8.6	39.1	38	13	BF137365	BF137365 603250066
C 830	8.8	40.0	50	9	AU104589	AU104589	AU104589	C 903	8.6	39.1	38	13	BF137365	BF137365 603250066
C 831	8.8	40.0	50	9	AU105003	AU105003	AU105003	C 904	8.6	39.1	38	17	AL771951	AL771951 Arabidops
C 832	8.8	40.0	50	9	AU105003	AU105003	AU105003	C 905	8.6	39.1	39	17	AZ324421	AL771951 Arabidops
C 833	8.8	40.0	50	9	AU105029	AU105029	AU105029	C 906	8.6	39.1	39	17	AZ324421	AZ324421 1M0046B22
C 834	8.8	40.0	50	9	AU105029	AU105029	AU105029	C 907	8.6	39.1	39	17	AZ324421	AZ324421 1M0046B22
C 835	8.8	40.0	50	9	AU105067	AU105067	AU105067	C 908	8.6	39.1	39	17	AZ514516	AZ514516 1M0361A12
C 836	8.8	40.0	50	9	AU105067	AU105067	AU105067	C 909	8.6	39.1	39	17	AZ514516	AZ514516 1M0361A12
C 837	8.8	40.0	50	9	AU105077	AU105077	AU105077	C 910	8.6	39.1	40	17	AZ390083	AZ514516 1M0361A12
C 838	8.8	40.0	50	9	AU105077	AU105077	AU105077	C 911	8.6	39.1	40	17	AZ390083	AZ390083 1M0151E17
C 839	8.8	40.0	50	9	AU105477	AU105477	AU105477	C 912	8.6	39.1	40	17	AZ829500	AZ390083 1M0151E17
C 840	8.8	40.0	50	9	AU105477	AU105477	AU105477	C 913	8.6	39.1	40	17	AZ829500	AZ829500 2M0107010
C 841	8.8	40.0	50	9	AU105478	AU105478	AU105478	C 914	8.6	39.1	41	13	BI548702	AZ829500 2M0107010
C 842	8.8	40.0	50	9	AU105478	AU105478	AU105478	C 915	8.6	39.1	41	13	BI548702	BI548702 603196881
C 843	8.8	40.0	50	9	AU105735	AU105735	AU105735	C 916	8.6	39.1	41	17	BH637243	BI548702 603196881
C 844	8.8	40.0	50	9	AU105735	AU105735	AU105735	C 917	8.6	39.1	42	14	D19980	BH637243 100801500
C 845	8.8	40.0	50	9	AU105828	AU105828	AU105828	C 918	8.6	39.1	42	14	D19980	D19980 HUMG00945
C 846	8.8	40.0	50	9	AU105828	AU105828	AU105828	C 919	8.6	39.1	43	9	A1084973	D19980 HUMG00945
C 847	8.8	40.0	50	9	AU105829	AU105829	AU105829	C 920	8.6	39.1	43	9	A1084973	A1084973 ow88a06.s
C 848	8.8	40.0	50	9	AU105829	AU105829	AU105829	C 921	8.6	39.1	43	9	A1789785	A1084973 ow88a06.s
C 849	8.8	40.0	50	9	AU105830	AU105830	AU105830	C 922	8.6	39.1	43	9	A1789785	A1789785 u153912.x
C 850	8.8	40.0	50	9	AU105830	AU105830	AU105830	C 923	8.6	39.1	43	9	A1790181	A1789785 u153912.x
C 851	8.8	40.0	50	9	AU105831	AU105831	AU105831	C 924	8.6	39.1	43	9	A1790181	A1790181 u154H05.x
C 852	8.8	40.0	50	9	AU107008	AU107008	AU107008	C 925	8.6	39.1	43	9	AA499553	A1790181 u154H05.x
C 853	8.8	40.0	50	9	AU107008	AU107008	AU107008	C 926	8.6	39.1	43	9	AA499553	AA499553 v194f08.r
C 854	8.8	40.0	50	9	AU107008	AU107008	AU107008	C 927	8.6	39.1	44	17	CNS07R95	AA499553 v194f08.r
C 855	8.8	40.0	50	9	AU107993	AU107993	AU107993	C 928	8.6	39.1	44	17	CNS07R95	AL680817 Anopheles
C 856	8.8	40.0	50	9	AU107993	AU107993	AU107993	C 929	8.6	39.1	44	13	BI906092	AL680817 Anopheles
C 857	8.8	40.0	50	12	BG148757	BG148757	BG148757	C 930	8.6	39.1	45	13	BI906092	BI906092 603062473
C 858	8.8	40.0	50	12	BG148757	BG148757	BG148757	C 931	8.6	39.1	45	13	BI906092	BI906092 603062473
C 859	8.8	40.0	50	12	BG569683	BG569683	BG569683	C 932	8.6	39.1	45	13	BI906092	BI906092 603062473
C 860	8.8	40.0	50	12	BG569683	BG569683	BG569683	C 933	8.6	39.1	45	13	BI906092	BI906092 603062473
C 861	8.8	40.0	50	17	AZ921856	AZ921856	AZ921856	C 934	8.6	39.1	45	17	AL753163	BI906092 603062473
C 862	8.8	40.0	50	17	AZ921856	AZ921856	AZ921856	C 935	8.6	39.1	45	17	AL753163	AL753163 Arabidops
C 863	8.6	39.1	25	17	AZ773296	AZ773296	AZ773296	C 936	8.6	39.1	48	17	TA372F02Q	AL753163 Arabidops
C 864	8.6	39.1	25	17	AZ773296	AZ773296	AZ773296	C 937	8.6	39.1	48	17	TA372F02Q	AL753163 Arabidops
C 865	8.6	39.1	27	14	D44905	D44905	D44905	C 938	8.6	39.1	49	9	AA123002	AL963310 T. brucei
C 866	8.6	39.1	27	14	D44905	D44905	D44905	C 939	8.6	39.1	49	9	AA123002	AA123002 mg23g11.r
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C 868	8.6	39.1	28	9	A1020682	A1020682	A1020682	C 941	8.6	39.1	49	9	A1457384	A1457384 t173c10.x
C 869	8.6	39.1	30	17	AL752337	AL752337	AL752337	C 942	8.6	39.1	49	9	A1875730	A1457384 t173c10.x
C 870	8.6	39.1	30	17	AL752337	AL752337	AL752337	C 943	8.6	39.1	49	9	A1875730	A1875730 u124D01.x
C 871	8.6	39.1	31	9	A1522965	A1522965	A1522965	C 944	8.6	39.1	49	14	W99572	A1875730 u124D01.x
C 872	8.6	39.1	31	9	A1522965	A1522965	A1522965	C 945	8.6	39.1	50	9	W99572	W99572 TGEESTz04F0
C 873	8.6	39.1	31	14	U44252	U44252	U44252	C 946	8.6	39.1	50	9	AU102731	W99572 TGEESTz04F0
C 874	8.6	39.1	31	14	U44252	U44252	U44252	C 947	8.6	39.1	50	9	AU102731	AU102731 AU102731
C 875	8.6	39.1	31	17	AZ785865	AZ785865	AZ785865	C 948	8.6	39.1	50	9	AU103186	AU102731 AU102731
C 876	8.6	39.1	31	17	AZ785865	AZ785865	AZ785865	C 949	8.6	39.1	50	9	AU103186	AU103186 AU103186
C 877	8.6	39.1	33	17	AZ479535	AZ479535	AZ479535	C 950	8.6	39.1	50	9	AU103244	AU103186 AU103186
C 878	8.6	39.1	33	17	AZ479535	AZ479535	AZ479535	C 951	8.6	39.1	50	9	AU103244	AU103244 AU103244
C 879	8.6	39.1	34	9	AA500126	AA500126	AA500126	C 952	8.6	39.1	50	9	AU103413	AU103244 AU103244
C 880	8.6	39.1	34	9	AA500126	AA500126	AA500126	C 953	8.6	39.1	50	9	AU103413	AU103413 AU103413
C 881	8.6	39.1	34	17	TA327F04Q	TA327F04Q	TA327F04Q	C 954	8.6	39.1	50	9	AU104342	AU103413 AU103413
C 882	8.6	39.1	34	17	TA327F04Q	TA327F04Q	TA327F04Q	C 955	8.6	39.1	50	9	AU104342	AU104342 AU104342

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C 959	8.6	39.1	50	9	AU106266	AU106266
C 960	8.6	39.1	50	9	AU106266	AU106266
C 961	8.6	39.1	50	9	AU106809	AU106809
C 962	8.6	39.1	50	9	AU106809	AU106809
C 963	8.6	39.1	50	9	AU106810	AU106810
C 964	8.6	39.1	50	9	AU106810	AU106810
C 965	8.6	39.1	50	9	AU106811	AU106811
C 966	8.6	39.1	50	9	AU106811	AU106811
C 967	8.6	39.1	50	9	AU106812	AU106812
C 968	8.6	39.1	50	9	AU106812	AU106812
C 969	8.6	39.1	50	9	AU106813	AU106813
C 970	8.6	39.1	50	9	AU106813	AU106813
C 971	8.6	39.1	50	9	AU106814	AU106814
C 972	8.6	39.1	50	9	AU106814	AU106814
C 973	8.6	39.1	50	9	AU106815	AU106815
C 974	8.6	39.1	50	9	AU106815	AU106815
C 975	8.6	39.1	50	9	AU106816	AU106816
C 976	8.6	39.1	50	9	AU106816	AU106816
C 977	8.6	39.1	50	9	AU106817	AU106817
C 978	8.6	39.1	50	9	AU106817	AU106817
C 979	8.6	39.1	50	9	AU106818	AU106818
C 980	8.6	39.1	50	9	AU106818	AU106818
C 981	8.6	39.1	50	9	AU106819	AU106819
C 982	8.6	39.1	50	9	AU106819	AU106819
C 983	8.6	39.1	50	9	AU106820	AU106820
C 984	8.6	39.1	50	9	AU106820	AU106820
C 985	8.6	39.1	50	9	AU106821	AU106821
C 986	8.6	39.1	50	9	AU106821	AU106821
C 987	8.6	39.1	50	9	AU106822	AU106822
C 988	8.6	39.1	50	9	AU106822	AU106822
C 989	8.6	39.1	50	9	AU107694	AU107694
C 990	8.6	39.1	50	9	AU107694	AU107694
C 991	8.6	39.1	50	9	AU107978	AU107978
C 992	8.6	39.1	50	9	AU107978	AU107978
C 993	8.6	39.1	50	10	AV956714	AV956714
C 994	8.6	39.1	50	10	AV956714	AV956714
C 995	8.6	39.1	50	17	BH790247	BH790247
C 996	8.6	39.1	50	17	BH790247	BH790247
C 997	8.4	38.2	22	17	AZ342067	AZ342067
C 998	8.4	38.2	22	17	HSMC03F05	HSMC03F05
C 999	8.4	38.2	23	17	HSMC03F05	HSMC03F05
C1000	8.4	38.2	23	17	HSMC03F05	HSMC03F05

ALIGNMENTS

RESULT 1
LOCUS A1749566 48 bp mRNA linear EST 22-JUN-1999
DEFINITION ac30f01.x1 Bartshead colon HPLRB7 Homo sapiens cDNA clone
IMAGE:2373529 3' similar to SW:RS29_HUMAN P30054 40S RIBOSOMAL
PROTEIN S29. ; mRNA sequence.
A1749566
ACCESSION A1749566.1 GI:5127830
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maira, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE Washu-NCI human EST project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

TEl: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 48
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2373529"
/clone_1b="Bartshead colon HPLRB7"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACGATCTGAAGTGGAGCGCCGCTTTTCTTTTCTTTTCTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
[5' AATCTACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Bartshead."

BASE COUNT 15 a 14 c 9 g 10 t
ORIGIN

Query Match 57.3%; Score 12.6; DB 9; Length 48;
Best Local Similarity 78.9%; Pred. No. 5.4e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 2 TGAGCCGATATCGCTTC 20
Db 10 TGAACCGATATCTTCGC 28

RESULT 2
LOCUS A1749566/c 48 bp mRNA linear EST 22-JUN-1999
DEFINITION ac30f01.x1 Bartshead colon HPLRB7 Homo sapiens cDNA clone
IMAGE:2373529 3' similar to SW:RS29_HUMAN P30054 40S RIBOSOMAL
PROTEIN S29. ; mRNA sequence.
A1749566
ACCESSION A1749566.1 GI:5127830
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maira, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE Washu-NCI human EST project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 48

FEATURES
SOURCE

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2373529"
/clone_1ib="Barstead colon HPLRB7"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/note="Organ: p771D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACGATCATCGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
[5', ATTCACTAGTAAT 3' and 5' ATTCACTAGT 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified p7713 vector. Library constructed by Bob
Barstead."

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	Query Match	Score	DB	Length
	Best Match Similarity	57.3%	12.6	48
	Best Local Similarity	78.9%	9	
	Matches	15	Pred. No. 5.4e+04	
		Conservative	0	Mismatches 4, Indels 0, Gaps 0;
Oy	3 GAGACCGATATCGGCTCTCA	21		
Db	28 GCGAGGATATCGGCTTCA	10		

RESULT 3	LOCUS	DEFINITION	VERSION	ACCESSION
AU103408	AU103408	50 bp mRNA	linear	EST 30-AUG-2001
	AU103408	Sugano Homo sapiens CDNA library	Homo sapiens	CDNA clone
	HEP00818	mRNA sequence.		
	AU103408			
	AU103408.1	GI:13552929		

ORGANISM	SOURCE
<i>Homo sapiens</i>	Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 50)	
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata	

TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072
COMMENT	Contact: Yutaka Suzuki

institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
5. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
location/Qualifiers
1. 50

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP0818"
/clone_1b="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT      3 a      14 g      12 t
ORIGIN

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Query Match	56.4%	Score 12.4	DB 9	Length 50
Best Local Similarity	72.7%	Pred. NO. 6.8e+04		
Matches 16	Conservative 0	Mismatches 6	Indels 0	Gaps 0
QY	1	CTGAGACCGATATCGGTCTCAG	22	

Db 24 CTCAGACCGTCGGCGTCTCTG 45

RESULT 4	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
AU103408/c	AU103408	50 bp mRNA linear EST 30-Aug-2001	AU103408	Sugano Homo sapiens cdna library Homo sapiens cdna clone	HEP000818, mRNA sequence.	human.
			AU103408.1	GI:13552929	EST.	human.

REFERENCE	1 (bases 1 to 50)
AUTHORS	Pammaraju, Polunovska, Primates, Catalinina, Hominidae, Homo. Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hatae , Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki , Y., Nakamura, Y., Sugama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
TITLE	EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL	21270072
MEDLINE	Contact: Yutaka Suzuki
COMMENT	

FEATURES

source	location/Qualifiers
1. 50	

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Suganoro S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

```

/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="HEP00818"
/clone_1b="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated u937 cells"
BASE COUNT      3 a      14 g      12 t
ORIGIN

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Query Match	56.4%;	Score 12.4;	DB 9;	Length 50;
Best Local Similarity	72.7%;	Pred. No. 6.8e+04;		
Matches 16; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	CTGAGACCGATATCGCTCTCAG	22	
	45	CAAGAGACCGCGCAGCGCTCTGAG	24	

RESULT 5	32 bp	DNA	linear	GSS 05-OCT-2000
LOCUS	AZ511046			
DEFINITION	1M0355120 Mouse 10kb plasmid UGCGIM library Mus musculus genomic			
ACCESSION	AZ511046			
VERSION	AZ511046.1	GI:10692362		

SOURCE	ORGANISM
house mouse.	
Mus musculus	
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus;	
1 (Passes 1 to 32)	
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duvall, B., Hamil, C.,	
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly	
, M., Rose, M., Rose, R., Stöck, R., Tinney, A., von Niederhausern, A.	

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL *PLoS ONE*
COMMENT Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY: University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0355 row: 1 column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.

FEATURES

SOURCE

1. .32
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0355120"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

14 a 4 c 3 g 11 t

ORIGIN

Query Match 54.5%; Score 12; DB 17; Length 32;
Best Local Similarity 75.0%; Pred. No. 9.2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATTCGCTCTCA 21
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6 TTAGACATATATAGCTCTCA 25

Db 6 TTAGACATATATAGCTCTCA 25

RESULT 6
AZ511046/c 32 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0355120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0355120 R, DNA sequence.

ACCESSION AZ511046
VERSION AZ511046.1 GI:10692362
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus.

REFERENCE 1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0355 row: 1 column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.

FEATURES

SOURCE

1. .32
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0355120"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

14 a 4 c 3 g 11 t

ORIGIN

Query Match 54.5%; Score 12; DB 17; Length 32;
Best Local Similarity 75.0%; Pred. No. 9.2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATTCGCTCTCA 21
|||||
25 TTAGACTTATATATGCTCTA 6

Db 25 TTAGACTTATATATGCTCTA 6

RESULT 7
N32567 37 bp mRNA linear EST 10-JAN-1996
LOCUS yw86605.s1 Soares placenta 809weeks 2NbHP809w Homo sapiens CDNA
DEFINITION clone IMAGE:259136.3' similar to gb:K52192 PROTO-ONCOGENE
TYROSINE-PROTEIN KINASE PES/FPS (HUMAN);, mRNA sequence.

ACCESSION N32567
VERSION N32567.1 GI:1152966
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 37)
Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marita, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston,
R., Williamson, A., Wohlmann, P., and Wilson, R.

TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine

JOURNAL

Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center

JOURNAL

Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: m13 -40 forward
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1.37
 /organism="Homo sapiens"
 /db_xref="GDB:388842"
 /db_xref="taxon:9606"
 /clone="IMAGE:259136"
 /clone_1lb="Soares_placenta_8to9weeks_2NBHP8to9W"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAGTGGAGCGCGCGCATTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."
 BASE COUNT 5 a 10 c 11 g 10 t 1 others
 ORIGIN

Query Match 54.5%; Score 12; DB 14; Length 37;
 Best Local Similarity 71.4%; Pred. NO. 9.6e+04;
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Yy 1 CTGAGACCGATATCGGTCTCA 21
 14 CTGATGCCGTTTCAGGCTCA 34

RESULT 8
 N32567/c
 LOCUS
 DEFINITION 37 bp mRNA linear EST 10-JAN-1996
 yw86e05.s1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens CDNA
 TYROSINE-PROTEIN KINASE FES/FPS (HUMAN); mRNA sequence.
 N32567
 N32567.1 GI:1152966
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 37)
 Hillier, L., Clark, N., Dubuque, T., Elliott, K., Hawkins, M., Holman
 'M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston
 'R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: m13 -40 forward
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1.37
 /organism="Homo sapiens"
 /db_xref="GDB:388842"
 /db_xref="taxon:9606"
 /clone="IMAGE:259136"
 /clone_1lb="Soares_placenta_8to9weeks_2NBHP8to9W"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAGTGGAGCGCGCGCATTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."
 BASE COUNT 5 a 10 c 11 g 10 t 1 others
 ORIGIN

Query Match 54.5%; Score 12; DB 14; Length 37;
 Best Local Similarity 71.4%; Pred. NO. 9.6e+04;
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Yy 2 TGAGACCGATATCGGTCTCAG 22
 34 TGAGCTGAANCGGATCAG 14

RESULT 9
 B1769009
 LOCUS
 DEFINITION 39 bp mRNA linear EST 25-SEP-2001
 603058167F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5207441 5',
 mRNA sequence.
 B1769009
 B1769009.1 GI:15760587
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 39)
 NIH-MGC http://imgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LAM11520 row: f column: 18
 High quality sequence stop: 39.
 Location/Qualifiers

FEATURES

source

1.39
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5207441"
 /clone_1lb="NIH_MGC_122"
 /lab_host="DH10B"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."

BASE COUNT

3 a 9 c 20 g 7 t

Query Match 54.5%; Score 12; DB 13; Length 39;

Best Local Similarity 75.0%; Pred. NO. 9.7e+04; Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGCTCTC 20
12 CTGCGACTGCTCTGCTCTC 31

RESULT 10
B1769009/c 39 bp mRNA linear EST 25-SEP-2001
LOCUS 603058167F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207441 5',
DEFINITION mRNA sequence.
VERSION B1769009
KEYWORDS B1769009.1 GI:15760587
SOURCE EST:
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 39)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L1AM1520 row: F column: 18
High quality sequence stop: 39.
Location/Qualifiers

FEATURES
source 1..39
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5207441"
/clone_1ib="NIH MGC_122"
/lab_host="MDH10B"
/note="Organ: pooled lung and spleen. Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."

BASE COUNT 3 a 9 c 20 g 7 t

Query Match 54.5%; Score 12; DB 13; Length 39;
Best Local Similarity 75.0%; Pred. NO. 9.7e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGCTCTCAG 22
31 GAGACCGACGACGACTCGCAG 12

RESULT 11
AUI06749 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI06749 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT05789, mRNA sequence.
VERSION AUI06749
KEYWORDS AUI06749.1 GI:13556270
SOURCE EST:
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J., Hata
H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K., Sakaki
Y., Nakamura.Y., Suyama.A. and Sugano.S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshimoto-Nakagawa.K., Maruyama.K., Suyama.A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES

source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT05789"
/clone_1ib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylsulfoxide treated U937 cells"
Location/Qualifiers

BASE COUNT

8 a 11 c 18 g 13 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. NO. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGCTCTCAG 22
5 GAGACCGATATGCTGCTTCG 24

RESULT 12
AUI06749 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI06749 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT05789, mRNA sequence.
VERSION AUI06749
KEYWORDS AUI06749.1 GI:13556270
SOURCE EST:
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J., Hata
H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K., Sakaki
Y., Nakamura.Y., Suyama.A. and Sugano.S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Source

1. .50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone.lib="KAT05789"
 /note="Differential display comparison of untreated and
 dimethylitumarate treated U937 cells"
 8 a 11 c 18 g 13 t

BASE COUNT

ORIGIN

Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 5;

Qy 1 CTGAGACCGATATCGTCTC 20
 |||||
 Db 24 CCGAGACGCTATCGTCTC 5

RESULT 13
 AUI07183 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07183 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF0623, mRNA sequence.

ACCESSION AUI07183
 VERSION AUI07183.1 GI:13556704
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 21270072

TITLE Contact: Yutaka Suzuki
 JOURNAL Department of Virology
 MEDLINE Institute of Medical Science, University of Tokyo
 COMMENT 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Source

1. .50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone.lib="COLF0623"
 /note="Differential display comparison of untreated and
 dimethylitumarate treated U937 cells"
 10 a 13 c 14 g 13 t

BASE COUNT

ORIGIN

Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 5;

Qy 1 CTGAGACCGATATCGTCTC 20
 |||||
 Db 20 CTGAGACGCTATCGTCTC 39

RESULT 14

AUI07183/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07183 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF0623, mRNA sequence.

ACCESSION AUI07183
 VERSION AUI07183.1 GI:13556704
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 21270072

TITLE Contact: Yutaka Suzuki
 JOURNAL Department of Virology
 MEDLINE Institute of Medical Science, University of Tokyo
 COMMENT 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES Location/Qualifiers
 Source 1. .50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone.lib="COLF0623"
 /note="Differential display comparison of untreated and
 dimethylitumarate treated U937 cells"
 10 a 13 c 14 g 13 t

BASE COUNT 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 5;

Qy 3 GAGACCGATATCGTCTCAG 22
 |||||
 Db 39 GTGACCCATCTGCTCTCAG 20

RESULT 15
 AUI07184 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07184 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF135, mRNA sequence.

ACCESSION AUI07184
 VERSION AUI07184.1 GI:13556705
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
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 EMBO Rep. 2 (5), 388-393 (2001)
 21270072

TITLE Contact: Yutaka Suzuki
 JOURNAL Department of Virology
 MEDLINE Institute of Medical Science, University of Tokyo
 COMMENT 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano

,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="COLF1135"
 /note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
 11 a 13 c 13 g 13 t

ORIGIN
 Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGTCTC 20
 |||||
 20 CTGAGCAGCATGCTGCTAC 39

RESULT 16
 AUI07184 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07184 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF1135, mRNA sequence.
 AUI07184
 VERSION AUI07184.1 GI:13556705
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

TITLE
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="COLF1135"
 /note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
 11 a 13 c 13 g 13 t

ORIGIN
 Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGTCTC 22
 |||||
 39 GTGACCATCTTGCTCTCAG 20

RESULT 17
 AUI07185 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07185 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF1135, mRNA sequence.
 AUI07185
 VERSION AUI07185.1 GI:13556706
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

TITLE
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

AUI07185 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HEP02932, mRNA sequence.
 AUI07185
 VERSION AUI07185.1 GI:13556706
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

TITLE
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEP02932"
 /note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
 11 a 13 c 13 g 13 t

ORIGIN
 Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGTCTC 20
 |||||
 21 CTGAGCAGCATGCTGCTAC 40

RESULT 18
 AUI07185 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07185 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION HEP02932, mRNA sequence.
 AUI07185
 VERSION AUI07185.1 GI:13556706
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

TITLE
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
Location/Qualifiers
1. .50
/db_xref="taxon:9606"
/clone="HEP02932"
/note="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATTCGCTCAG 22
Db 40 GTGACCATCTGCTCTCAG 21

RESULT 19
LOCUS AU107188 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU107188 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AU107188
VERSION AU107188
KEYWORDS GI:13556709
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL Contact: Yutaka Suzuki
MEDLINE Department of Virology
COMMENT Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. .50
/db_xref="taxon:9606"
/clone="LNG05625"
/note="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT
10 a 14 c 11 g 15 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCATTCGCTCAG 20
Db 26 CTGAGAGCAGATGGTCTAC 45

RESULT 20
LOCUS AU107188 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU107188 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AU107188
VERSION AU107188
KEYWORDS LNG05625, mRNA sequence.

ACCESSION AU107188
VERSION AU107188.1 GI:13556709
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL Contact: Yutaka Suzuki
MEDLINE Department of Virology
COMMENT Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. .50
/db_xref="taxon:9606"
/clone="LNG05625"
/note="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT
10 a 14 c 11 g 15 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATTCGCTCAG 22
Db 45 GTGACCATCTGCTCTCAG 26

RESULT 21
LOCUS AU107189 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU107189 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION KAI14023, mRNA sequence.
AU107189
VERSION AU107189.1 GI:13556710
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL Contact: Yutaka Suzuki
MEDLINE Department of Virology
COMMENT Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. .50

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAI1A4023"
/note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
ORIGIN
10 a 12 c 13 g 15 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1 CTGAGCCGATATCGTCTC 20
22 CTGAGCCGATATCGTCTAC 41

RESULT 22
AUI07189/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI07189 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KIAA4023, mRNA sequence.
ACCESSION AUI07189
VERSION AUI07189.1 GI:13556710
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tanoda, T., Mitsuhashi-Sugano, J., Sese, J., Hara
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuk@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAI1A4023"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"

BASE COUNT
ORIGIN
10 a 12 c 13 g 15 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 3 GAGACCGATATCGTCTCAG 22
41 GTGACCATCTTCTCTCAG 22

RESULT 23
AUI013431 32 bp mRNA linear EST 03-AUG-1998
LOCUS AUI013431 Schizosaccharomyces pombe late log phase cDNA
DEFINITION Schizosaccharomyces pombe cDNA clone spc08150, mRNA sequence.
ACCESSION AUI013431
VERSION AUI013431.1 GI:3368222

KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 32)
Moriyomo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
Location/Qualifiers
1..32
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08150"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19. The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL: <http://www.nirs.go.jp>)"

BASE COUNT
ORIGIN
11 a 5 c 11 g 4 t

Query Match 53.6%; Score 11.8; DB 9; Length 32;
Best Local Similarity 81.2%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 GAGACCGATATCGTCTC 18
3 GAGACCGATATCGGAC 18

RESULT 24
AUI013431/c 32 bp mRNA linear EST 03-AUG-1998
LOCUS AUI013431 Schizosaccharomyces pombe late log phase cDNA
DEFINITION Schizosaccharomyces pombe cDNA clone spc08150, mRNA sequence.
ACCESSION AUI013431
VERSION AUI013431.1 GI:3368222
KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 32)
Moriyomo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
Location/Qualifiers
1..32
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08150"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"

/note="Vector: M13mp19, The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 11 a 5 c 11 g 4 t 1 others

ORIGIN

Query Match 53.6%; Score 11.8; DB 9; Length 32;
Best Local Similarity 81.2%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GACGATATCGCTCTC 20
18 GTNCGCTATCGCTCTC 3

Db 18 GTNCGCTATCGCTCTC 3

RESULT 25
BH805089 42 bp DNA linear GSS 25-APR-2002
LOCUS 1008065D09.1EL_Y1 1008 - Rescuemu Grid I Zea mays genomic, DNA
DEFINITION sequence.
ACCESSION BH805089.1 GI:20322013
VERSION BH805089
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 42)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon
Unpublished (2001)
Contact: Walbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008065 column: 23
Class: transposon-tagged.
Location/Qualifiers

FEATURES
source
1..42
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - Rescuemu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site www.zmdb.iastate.edu and follow the links for 'Rescuemu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 13 c 9 g 9 t

ORIGIN

Query Match 53.6%; Score 11.8; DB 17; Length 42;
Best Local Similarity 86.7%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CCGATATCGCTCTCA 21
19 CCGATCTCGCTCTCA 33

Db 19 CCGATCTCGCTCTCA 33

RESULT 26
BH805089/c 42 bp DNA linear GSS 25-APR-2002
LOCUS 1008065D09.1EL_Y1 1008 - Rescuemu Grid I Zea mays genomic, DNA
DEFINITION sequence.
ACCESSION BH805089.1 GI:20322013
VERSION BH805089
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 42)
Walbot, V.
Maize genomic sequences found using engineered Rescuemu transposon
Unpublished (2001)
Contact: Walbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008065 column: 23
Class: transposon-tagged.
Location/Qualifiers

FEATURES
source
1..42
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - Rescuemu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site www.zmdb.iastate.edu and follow the links for 'Rescuemu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 13 c 9 g 9 t

ORIGIN

Query Match 53.6%; Score 11.8; DB 17; Length 42;
Best Local Similarity 86.7%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGAGACGATATCGG 16
33 TGAGACGAGATCGG 19

Db 33 TGAGACGAGATCGG 19

RESULT 27
AZ304932 43 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0005G03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0005G03 F, DNA sequence.
ACCESSION AZ304932

VERSION AZ304932.1 GI:10341444
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: G column: 03
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
1. 43
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U96100005G03"
/clone_lib="Mouse 10kb plasmid U96100005G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1/4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 9 c 9 g 12 t
ORIGIN

Query Match 53.6%; Score 11.8; DB 17; Length 43;
Best Local Similarity 86.7%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGCGATATCG 15
| | | | | | | | | | | | | | | | |
Db 8 CTGAGCGATATG 22

RESULT 28
AZ304932/c 43 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0005G03F Mouse 10kb plasmid U96100005G03
DEFINITION clone U96100005G03 F, DNA sequence.
ACCESSION AZ304932

VERSION AZ304932.1 GI:10341444
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: G column: 03
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
1. 43
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U96100005G03"
/clone_lib="Mouse 10kb plasmid U96100005G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1/4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 13 a 9 c 9 g 12 t
ORIGIN

Query Match 53.6%; Score 11.8; DB 17; Length 43;
Best Local Similarity 86.7%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGATATCGTCTCAG 22
| | | | | | | | | | | | | | | | |
Db 22 CTATATCGTCTCAG 8

RESULT 29
A1003871 48 bp mRNA linear EST 27-AUG-1998
LOCUS 0c46c06.s1 Soares testis NHT Homo sapiens cDNA IMAGE:1619818
DEFINITION 3' similar to gb:M5531 GALACTOSIDE 2-L-FUCOSYLTRANSFERASE (HUMAN); contains MER14.b1 MER14 repetitive element ;, mRNA sequence.

ACCESSION AI003871
VERSION AI003871.1 GI:3213381
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrip/image/image.html

FEATURES
source
1. 48
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1619818"
/clone_id="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTITTTTITTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
10 a 4 c 8 g 26 t

ORIGIN
Query Match 52.7%; Score 11.6; DB 9; Length 48;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGAGACGATTCGCTCT 19
|||||
Db 29 TGAGACGATTCGCTCT 46
|||||

RESULT 30
AI003871/c 48 bp mRNA linear EST 27-AUG-1998
LOCUS 064606.01 Soares_testis_NHT Homo sapiens CDNA clone IMAGE:1619818
DEFINITION 3' similar to gp:M5531 GALACTOSIDE 2-L-FUCOSYLTRANSFERASE (HUMAN)
ACCESSION AI003871
VERSION AI003871.1 GI:3213381
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrip/image/image.html

FEATURES
source
1. 48
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1619818"
/clone_id="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTITTTTITTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
10 a 4 c 8 g 26 t

ORIGIN
Query Match 52.7%; Score 11.6; DB 9; Length 48;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGACGATTCGCTCTCA 21
|||||
Db 46 AGACGATTCGCTCTCA 29
|||||

RESULT 31
AI07186 50 bp mRNA linear EST 30-AUG-2001
LOCUS AI07186 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
DEFINITION KAT09043, mRNA sequence.
ACCESSION AI07186
VERSION AI07186.1 GI:13556707
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

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FEATURES
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      /db_xref="taxon:9606"
      /clone="KAT09043"
      /note="Differential display comparison of untreated and
      dimethylflumarate treated U937 cells"
BASE COUNT
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  13 g
  15 t

Query Match
  52.7%; Score 11.6; DB 9; Length 50;
  Best Local Similarity 77.8%; Pred. No. 1.6e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
  1 CTGAGACCGATATCGCTC 18
  |||||
  20 CTGAGACCAAGATGGCTC 37

RESULT 32
AU017186/c
AU017186/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION
  AU017186 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
  KAT09043, mRNA sequence.
ACCESSION
  AU017186
VERSION
  AU017186.1 GI:13556707
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  Suzuki,Y., Taira,H., Tsunoda,T., Mitsuhashi-Sugano,J., Sese,J., Hata
  H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
  Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
  EMBO Rep. 2 (5), 388-393 (2001)
  21270072
JOURNAL
  Contact: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
  Email: yusuzuki@ims.u-tokyo.ac.jp
  Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
  S. Construction and characterization of a full length-enriched and
  a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
  Location/Qualifiers
    1..50
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    /db_xref="taxon:9606"
    /clone="KAT09043"
    /note="Differential display comparison of untreated and
    dimethylflumarate treated U937 cells"
BASE COUNT
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  11 c
  13 g
  15 t

Query Match
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  Best Local Similarity 77.8%; Pred. No. 1.6e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
  5 GACCGATATCGCTCNG 22
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  37 GACCGATATCGCTCNG 20

Db
  37 GACCGATATCGCTCNG 20

RESULT 33
AU013455
AU013455 32 bp mRNA linear EST 03-AUG-1998
LOCUS
  AU013455 Schizosaccharomyces pombe late log phase cDNA
  Schizosaccharomyces pombe cDNA clone spc08177, mRNA sequence.
  Schizosaccharomyces pombe cDNA clone spc08177, mRNA sequence.

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ACCESSION
  AU013455
  AU013455.1 GI:3368246
KEYWORDS
  EST.
SOURCE
  fission yeast.
ORGANISM
  Schizosaccharomyces pombe
  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
  Schizosaccharomycetales; Schizosaccharomycetaceae;
  Schizosaccharomycetes.
  1 (bases 1 to 32)
REFERENCE
  Moriyomo,M. and Mita,K.
  Identification of expressed sequence tags of Schizosaccharomyces
  pombe
  Unpublished (1998)
JOURNAL
  Contact: Mitsunori Moriyomo
  Genome Research Group
  National Institute of Radiological Sciences
  9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
  Email: moriyomo@nirs.go.jp.
  Location/Qualifiers
    1..32
    /organism="Schizosaccharomyces pombe"
    /strain="972"
    /db_xref="taxon:4896"
    /clone="spc08177"
    /clone_1lb="Schizosaccharomyces pombe late log phase cDNA"
    /sex="h minus"
    /note="Vector: M13mp19. The cDNA library of
    Schizosaccharomyces pombe was prepared by cloning cDNA
    into the SmaI site of M13mp19 DNA and the direction of DNA
    sequences was not always from 5' to 3'. The cDNA data of
    Schizosaccharomyces pombe are available for searching on
    the World Wide Web. (URL: http://www.nirs.go.jp)"
BASE COUNT
  12 a
  12 c
  11 g
  11 t
  5 c
  3 t
  1 others

Query Match
  51.8%; Score 11.4; DB 9; Length 32;
  Best Local Similarity 92.3%; Pred. No. 1.8e+05;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  3 GAGACCGATATCG 15
  |||||
  3 GAGACCGATATGCG 15

Db
  3 GAGACCGATATGCG 15

RESULT 34
AU013455/c
AU013455/c 32 bp mRNA linear EST 03-AUG-1998
LOCUS
  AU013455 Schizosaccharomyces pombe late log phase cDNA
  Schizosaccharomyces pombe cDNA clone spc08177, mRNA sequence.
  Schizosaccharomyces pombe cDNA clone spc08177, mRNA sequence.
ACCESSION
  AU013455
VERSION
  AU013455.1 GI:3368246
KEYWORDS
  EST.
SOURCE
  fission yeast.
ORGANISM
  Schizosaccharomyces pombe
  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
  Schizosaccharomycetales; Schizosaccharomycetaceae;
  Schizosaccharomycetes.
  1 (bases 1 to 32)
REFERENCE
  Moriyomo,M. and Mita,K.
  Identification of expressed sequence tags of Schizosaccharomyces
  pombe
  Unpublished (1998)
JOURNAL
  Contact: Mitsunori Moriyomo
  Genome Research Group
  National Institute of Radiological Sciences
  9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
  Email: moriyomo@nirs.go.jp.
  Location/Qualifiers
    1..32
    /organism="Schizosaccharomyces pombe"
    /strain="972"
    /db_xref="taxon:4896"
    /clone="spc08177"

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clone.lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.ntrs.go.jp)"
BASE COUNT      12 a       5 c       11 g       3 t       1 others
ORIGIN
Query Match      51.8%; Score 11.4; DB 9; Length 32;
Best Local Similarity 92.3%; Pred. NO.1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY               8 CGATATCGGTCTC 20
                |||||
                |||||
Db              15 CGCATTCGATCTC 3
RESULT 35
LOCUS            AU013784                      34 bp mRNA linear EST 03-AUG-1998
DEFINITION      AU013784 Schizosaccharomyces pombe late log phase cDNA
ACCESSION      AU013784
VERSION        AU013784.1 GI:3368575
KEYWORDS
SOURCE         fission yeast.
ORGANISM       Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE       1 (bases 1 to 34)
AUTHORS        Morimyo,M. and Mita,K.
TITLE          Identification of expressed sequence tags of Schizosaccharomyces
pombe
JOURNAL        Unpublished (1998)
COMMENT        Contact: Mitsuki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
FEATURES             source
     1..34
     /organism="Schizosaccharomyces pombe"
     /strain="972"
     /db_xref="taxon:4896"
     /clone="spc08658"
     /clone.lib="Schizosaccharomyces pombe late log phase cDNA"
     /sex="h minus"
     /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.ntrs.go.jp)"
BASE COUNT      12 a       6 c       12 g       4 t
ORIGIN
Query Match      51.8%; Score 11.4; DB 9; Length 34;
Best Local Similarity 92.3%; Pred. NO.1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY               3 GAGACCGATTGCG 15
                |||||
                |||||
Db              5 GAGACCGATTGCG 17
RESULT 36
LOCUS            AU013784                      34 bp mRNA linear EST 03-AUG-1998
DEFINITION      AU013784 Schizosaccharomyces pombe late log phase cDNA
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ACCESSION	Schizosaccharomyces pombe cDNA clone spc08658, mRNA sequence.	
VERSION	AU013784	
KEYWORDS	EST.	
SOURCE	fission yeast.	
ORGANISM	Schizosaccharomyces pombe	
JOURNAL	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	
COMMENT	Schizosaccharomycetales; Schizosaccharomycetaceae;	
REFERENCE	Schizosaccharomyces.	
AUTHORS	1 (bases 1 to 34)	
TITLE	Moriyomo, M. and Mita, K.	
	Identification of expressed sequence tags of Schizosaccharomyces	
	pombe	
	Unpublished (1998)	
	Contact: Mitsuoki Moriyomo	
	Genome Research Group	
	National Institute of Radiological Sciences	
	9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan	
	Email: moriyomo@nirs.go.jp	
FEATURES	Location/Qualifiers	
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	/strain="972"	
	/db_xref="taxon:4896"	
	/clone="spc08658"	
	/clone_id="Schizosaccharomyces pombe late log phase cDNA"	
	/sex="h minus"	
	/note="Vector: M13mp19; The cDNA library of	
	Schizosaccharomyces pombe was prepared by cloning cDNA	
	into the SmaI site of M13mp19 DNA and the direction of DNA	
	sequences was not always from 5' to 3'. The cDNA data of	
	Schizosaccharomyces pombe are available for searching on	
	the World Wide Web. (URL, http://www.nirs.go.jp)"	
BASE COUNT	12 a 6 c 12 g 4 t	
ORIGIN		
Query Match	51.8%; Score 11.4; DB 9; Length 34;	
Best Local Similarity	92.3%; Pred. No. 1.8e+05;	
Matches 12; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	8 CGATATCGGTCTC 20	
Db	17 CGCTATCGGTCTC 5	
RESULT 37		
LOCUS	AU013851 34 bp mRNA linear EST 03-AUG-1998	
DEFINITION	AU013851 Schizosaccharomyces pombe late log phase cDNA	
ACCESSION	Schizosaccharomyces pombe cDNA clone spc08749, mRNA sequence.	
VERSION	AU013851	
KEYWORDS	AU013851.1 GI:3368642	
SOURCE	EST.	
ORGANISM	fission yeast.	
	Schizosaccharomyces pombe	
	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	
	Schizosaccharomycetales; Schizosaccharomycetaceae;	
	Schizosaccharomyces.	
	1 (bases 1 to 34)	
	Moriyomo, M. and Mita, K.	
	Identification of expressed sequence tags of Schizosaccharomyces	
	pombe	
	Unpublished (1998)	
	Contact: Mitsuoki Moriyomo	
	Genome Research Group	
	National Institute of Radiological Sciences	
	9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan	
	Email: moriyomo@nirs.go.jp	
	Location/Qualifiers	
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	/strain="972"	
	/db_xref="taxon:4896"	

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/clone="spc08749"
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/sex="h minus"
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Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT      12 a      6 c      12 g      4 t
ORIGIN
Query Match      51.8%; Score 11.4; DB 9; Length 34;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      3 GAGACCGATATCG 15
      |||||
      5 GAGACCGATACGC 17
DB
RESULT 38
AU013851/c      34 bp mRNA linear EST 03-AUG-1998
LOCUS
DEFINITION AU013851 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU013851
VERSION AU013851
KEYWORDS
SOURCE EST.
ORGANISM fission yeast.
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 34)
Moriyomo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
Unpublished (1998)
Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
Location/Qualifiers
1..34
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Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT      12 a      6 c      12 g      4 t
ORIGIN
Query Match      51.8%; Score 11.4; DB 9; Length 34;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      8 CGATATCGGTC 20
      |||||
      17 CGGATCGGTC 5
DB
RESULT 39
AV833036
LOCUS
AV833036      38 bp mRNA linear EST 22-JUN-2001

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DEFINITION	AVB33036 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA clone bags10c17, mRNA sequence.			
ACCESSION	AVB33036			
VERSION	AVB33036.1 GI:14525125			
KEYWORDS	EST.			
SOURCE	Hordeum vulgare subsp. vulgare.			
ORGANISM	Hordeum vulgare subsp. vulgare			
REFERENCE	Sato, K. 1 (bases 1 to 38)			
AUTHORS	Sato, K.			
TITLE	Barley EST sequencing project in NIG and Okayama Univ			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Kazuhiro Sato Research Institute for Bioreources Okayama University, Barley Germplasm Center Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan Email: kazsato@rib.okayama-u.ac.jp/ URL: http://www.rib.okayama-u.ac.jp/barley/ Sato, K., Saitsho, D., Takeda, K., Shim, T. and Kohara, Y. Direct submission: database: http://www.shigen.nig.ac.jp/barley/barley.html. Location/Qualifiers 1. 38 /organism="Hordeum vulgare subsp. vulgare" /cultivar="Haruna Nijo" /db_xref="taxon:112509" /clone="bags10c17" /clone_1lb="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination" /cissue_type="shoots" /dev_stage="germination" 11 a 8 c 11 t			
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Best Local Similarity	92.3%	Pred. No.	1.8e+05;	
Matches	12;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
Oy	9 GATATCGGTCTCA 21 13 GATATCGGTCTCA 25			
Db	13 GATATCGGTCTCA 25			
RESULT 40				
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LOCUS	AVB33036 38 bp mRNA linear EST 22-JUN-2001			
DEFINITION	AVB33036 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA clone bags10c17, mRNA sequence.			
ACCESSION	AVB33036			
VERSION	AVB33036.1 GI:14525125			
KEYWORDS	EST.			
SOURCE	Hordeum vulgare subsp. vulgare.			
ORGANISM	Hordeum vulgare subsp. vulgare			
REFERENCE	Sato, K. 1 (bases 1 to 38)			
AUTHORS	Sato, K.			
TITLE	Barley EST sequencing project in NIG and Okayama Univ			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Kazuhiro Sato Research Institute for Bioreources Okayama University, Barley Germplasm Center Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan Email: kazsato@rib.okayama-u.ac.jp/ URL: http://www.rib.okayama-u.ac.jp/barley/ Sato, K., Saitsho, D., Takeda, K., Shim, T. and Kohara, Y. Direct submission: database: http://www.shigen.nig.ac.jp/barley/barley.html. Location/Qualifiers 1. 38 /organism="Hordeum vulgare subsp. vulgare" /cultivar="Haruna Nijo" /db_xref="taxon:112509" /clone="bags10c17" /clone_1lb="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination" /cissue_type="shoots" /dev_stage="germination" 11 a 8 c 11 t			

FEATURES
source

Location/Qualifiers
1. .38
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/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="bags10c17"
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vulgare subsp. vulgare shoots germination"
/issue_type="shoots"
/dev_stage="germination"
BASE COUNT 11 a 8 c 8 g 11 t
ORIGIN

Query Match 51.8%; Score 11.4; DB 10; Length 38;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCGATATC 14
|||||
Db 25 TGAGACCGATATC 13

Search completed: June 14, 2003, 22:37:59
Job time : 1390 secs

